

CONTIG2667	1203416_c2_9 1203416_c2_9	3563	17666	264	88	YDR079W	214	1.3(10)-17	Saccharomyces cerevisiae	[ui:ydr079w] [pn:cytochrome c oxidase assembly protein:hypothetical 13.2 kd protein in sed1-pdc2 intergenic region] [gn:pet100:d4441] [gtcf:2.8:12.16] [keggf:14.2] [sgdf:2.5:0.6:4.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1205	23478430_f1_1	3564	17667	465	155	YDR120C	160	2.0(10)-22	Saccharomyces cerevisiae	[ui:ydr120c] [pn:n2,n2-dimethylguanine tma methyltransferase:n2,n2-dimethylguanosine tma methyltransferase precursor] [gn:trm1-yd9727] [gtcf:2.8:10.6] [ec:2.1.1.32] [keggf:14.1] [sgdf:4.6:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG645	15829015_c3_3	3565	17668	744	248	YDR120C	646	2.1(10)-63	Saccharomyces cerevisiae	[ui:ydr120c] [pn:n2,n2-dimethylguanine tma methyltransferase:n2,n2-dimethylguanosine tma methyltransferase precursor] [gn:trm1-yd9727] [gtcf:2.8:10.6] [ec:2.1.1.32] [keggf:14.1] [sgdf:4.6:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5076	1203416_c2_9	3566	17669	2013	671	YDR194C	524	1.8(10)-50	Saccharomyces cerevisiae	[ui:ydr194c] [pn:ma helicase of the dead box family, mitochondrial:atp-dependent ma helicase mss116 precursor] [gn:mss116:ydr9346] [gtcf:2.8:10.2] [keggf:14.2] [sgdf:4.9:0.9:7.0] [db:gtc-saccharomyces cerevisiae]

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CONTIG4689	22298761_c3_11	3567	17670	564	188	YDR197W	139	6.7(10)-9	Saccharomyces cerevisiae	[ui:ydr197w] [pn:cytochrome b translational activator protein:cytochrome b translational activator protein cbs2] [gn:cbs2:cbp7:ydr346] [gicf:2.8:10.7] [keggf:1.4.2] [sgdgc:5.3:0.9:7.0] [db:gic-saccharomyces cerevisiae]
CONTIG3239	995667_c2_7	3568	17671	711	237	YDR232W	715	1.0(10)-70	Saccharomyces cerevisiae	[ui:ydr232w] [pn:5-aminolevulinate synthase:5-aminolevulinic acid synthase, mitochondrial precursor:delta-aminolevulinate synthase:delta-ala synthetase] [gn:hem1:ydr9934] [gicf:2.8:5.3:9.10:9.11] [ec:2.3.1.37] [keggf:5.3] [sgdgc:1.7]
CONTIG3239	9882667_c1_5	3569	17672	930	310	YDR232W	945	4.2(10)-95	Saccharomyces cerevisiae	[ui:ydr232w] [pn:5-aminolevulinate synthase:5-aminolevulinic acid synthase, mitochondrial precursor:delta-aminolevulinate synthase:delta-ala synthetase] [gn:hem1:ydr9934] [gicf:2.8:5.3:9.10:9.11] [ec:2.3.1.37] [keggf:5.3] [sgdgc:1.7]
CONTIG4672	21640811_c1_8	3570	17673	1158	386	YDR234W	97	0.13	Saccharomyces cerevisiae	[ui:ydr234w] [pn:homoaconitase:homoaconitase precursor:homoaconitate hydratase] [gn:lys4:ydr9934] [gicf:2.8:5.8:6.6] [ec:4.2.1.36] [keggf:5.8] [sgdgc:1.1:9.7.0] [db:gic-saccharomyces cerevisiae]

CONTIG4880	34703879_c1_6	3571	17674	1977	659	YDR234W	2353	2.7(10)-244	Saccharomyces cerevisiae	[ui:ydr234w] [pn:homoaconitase:homoaconitase precursor:homoaconitase hydratase] [gn:lys4:ydr9934] [gtcf:2.8:5.8:6.6] [ec:4.2.1.36] [keggfc:5.8] [sgdfc:1.1:1.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5547	13787567_c3_17	3572	17675	2328	776	YDR258C	2282	9.0(10)-237	Saccharomyces cerevisiae	[ui:ydr258c] [pn:heat shock protein of clpb family of atp-dependent proteases, mitochondrial:mitochondrial heat shock protein 78 precursor] [gn:hsp78] [gtcf:12.7:2.8:10.11:13.2] [keggfc:14.2] [sgdfc:6.0:9.7:0:1.1.0] [db:gtc-saccha]
CONTIG5125	24414078_c2_14	3573	17676	1215	405	YDR268W	977	1.8(10)-98	Saccharomyces cerevisiae	[ui:ydr268w] [pn:tryptophanyl-trna synthetase, mitochondrial:tryptophan--trna ligase:trps] [gn:msw1:msw:d9954] [gtcf:2.8:5.14:10.6] [ec:6.1.1.2] [keggfc:5.14:10.1:10.2] [sgdfc:5.4:0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5518	9765627_c3_20	3574	17677	1047	349	YDR337W	439	1.8(10)-41	Saccharomyces cerevisiae	[ui:ydr337w] [pn:ribosomal protein of the small subunit, mitochondrial:mitochondrial 40s ribosomal protein s28 precursor] [gn:mmps28:d9651] [gtcf:2.8:10.4] [keggfc:14.2] [sgdfc:5.1:0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4636	501381_f3_2	3575	17678	1077	359	YDR347W	163	5.9(10)-10	Saccharomyces cerevisiae	[ui:ydr347w] [pn:ribosomal protein of the small subunit, mitochondrial:mitochondrial 40s ribosomal protein mrp1] [gn:mrp1:d9651] [gtcf:2.8:10.4] [keggf:14.2] [sgdf:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2236	21650937_f1_1	3576	17679	627	209	YDR375C	795	3.3(10)-79	Saccharomyces cerevisiae	[ui:ydr375c] [pn:mitochondrial protein of the cdc48/pas1/sec18:aaa family of atpases:bes1 protein] [gn:bes1:d9481] [gtcf:2.8:12.16] [keggf:14.2] [sgdf:6.4:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4291	16836540_f2_3	3577	17680	309	103	YDR375C	118	1.7(10)-6	Saccharomyces cerevisiae	[ui:ydr375c] [pn:mitochondrial protein of the cdc48/pas1/sec18:aaa family of atpases:bes1 protein] [gn:bes1:d9481] [gtcf:2.8:12.16] [keggf:14.2] [sgdf:6.4:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3826	11038567_c2_3	3578	17681	813	271	YDR376W	345	1.6(10)-31	Saccharomyces cerevisiae	[ui:ydr376w] [pn:similarity to human adrenodoxin reductase and ferredoxin-nadp+ reductase:nadph:adrenodoxin oxidoreductase homolog precursor:adrenodoxin reductase homolog] [gn:arh1:d9481] [gtcf:2.8:3.4:8.1:8.2] [keggf:14.2] [sgdf:1]

CONTIG1088	22378775_f3_1	3579	17682	609	203	YDR405W	279	1.6(10)-24	Saccharomyces cerevisiae	[ui:ydr405w] [pn:ribosomal protein of the large subunit, mitochondrial:mitochondrial 60s ribosomal protein l41 precursor:ym141] [gn:mrp141:mrp20:d9509] [gtcf:2.8:10.4] [keggf:14.2] [sgdfc:5.1.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2510	6640687_f1_1	3580	17683	495	165	YDR462W	316	1.8(10)-28	Saccharomyces cerevisiae	[ui:ydr462w] [pn:ribosomal protein yml28, mitochondrial] [gtcf:2.8:10.4] [keggf:14.2] [sgdfc:5.1.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2838	4085965_c2_4	3581	17684	960	320	YER014W	327	3.7(10)-29	Saccharomyces cerevisiae	[ui:yer014w] [pn:protoporphyrinogen oxidase, mitochondrial:protoporphyrinogen oxidase:ppo] [gn:hem14] [gtcf:2.8:9.10:9.11] [ec:1.3.3.4] [keggf:9.10] [sgdfc:1.7.1:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5244	10156251_f3_10	3582	17685	621	207	YER014W	379	4.0(10)-35	Saccharomyces cerevisiae	[ui:yer014w] [pn:protoporphyrinogen oxidase, mitochondrial:protoporphyrinogen oxidase:ppo] [gn:hem14] [gtcf:2.8:9.10:9.11] [ec:1.3.3.4] [keggf:9.10] [sgdfc:1.7.1:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1007	24320317_t2_1	3583	17686	855	285	YER017C	575	7.0(10)-56	Saccharomyces cerevisiae	[ui:yer017c] [pn:protease of the sec18/cdc48/pas1 family of atpases:aaa:afg3 protein:tat-binding homolog 10] [gn:afg3:yta10] [gtcf:2.8:10.11:12.16] [ec:3.4.24.-] [keggfc:14.1] [sgdfc:6.4.0:6.5:3.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5132	24508438_c2_11	3584	17687	1209	403	YER017C	959	4.5(10)-126	Saccharomyces cerevisiae	[ui:yer017c] [pn:protease of the sec18/cdc48/pas1 family of atpases:aaa:afg3 protein:tat-binding homolog 10] [gn:afg3:yta10] [gtcf:2.8:10.11:12.16] [ec:3.4.24.-] [keggfc:14.1] [sgdfc:6.4.0:6.5:3.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG385	11750755_c3_4	3585	17688	687	229	YER026C	708	5.5(10)-70	Saccharomyces cerevisiae	[ui:yer026c] [pn:cdp-diacylglycerol serine o-phosphatidyltransferase:cdp-diacylglycerol--serine o-phosphatidyltransferase:phosphatidylserine synthase] [gn:chol:pss1:pss] [gtcf:2.8:3.4:5.3:8.1:8.2:12.16] [ec:2.7.8.8] [keggfc:5.3:8.1]
CONTIG2766	10632776_c2_6	3586	17689	306	102	YER058W	128	1.6(10)-8	Saccharomyces cerevisiae	[ui:yer058w] [pn:cytochrome c oxidase assembly factor:protein precursor] [gn:pet117] [gtcf:2.8:12.16] [keggfc:14.2] [sgdfc:6.4.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4186	6647807_f3_2	3587	17690	924	308	YER061C	534	1.5(10)-51	Saccharomyces cerevisiae	[ui:yer061c] [pn:3-oxoacyl-acyl-carrier-protein synthase homolog:beta-keto-acyl-acp synthase, mitochondrial] [gn:cem1] [gtcf:2.8.3.1.3.4.8.1:8.2] [ec:2.3.1.41] [keggfc:3.1] [sgdfc:1.6.1:2.5.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4985	20897942_c3_9	3588	17691	282	94	YER061C	220	1.2(10)-17	Saccharomyces cerevisiae	[ui:yer061c] [pn:3-oxoacyl-acyl-carrier-protein synthase homolog:beta-keto-acyl-acp synthase, mitochondrial] [gn:cem1] [gtcf:2.8.3.1.3.4.8.1:8.2] [ec:2.3.1.41] [keggfc:3.1] [sgdfc:1.6.1:2.5.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5605	486575_f1_2	3589	17692	2598	866	YER069W	2780	1.5(10)-289	Saccharomyces cerevisiae	[ui:yer069w] [pn:acetylglutamate kinase and acetylglutamyl-phosphate reductase] [gn:arg5:6] [gtcf:2.8.6.6] [keggfc:14.2] [sgdfc:1.1.1:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4952	26270942_c3_8	3590	17693	660	220	YER086W	671	4.7(10)-66	Saccharomyces cerevisiae	[ui:yer086w] [pn:anabolic serine and threonine dehydratase precursor:threonine deaminase] [gn:ilv1] [gtcf:2.8.5.3:6.6] [ec:4.2.1.16] [keggfc:5.3] [sgdfc:1.1.1:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5168	32209802_fl_2	3591	17694	582	194	YER086W	565	8.0(10)-55	Saccharomyces cerevisiae	[ui:yer086w] [pn:anabolic serine and threonine dehydratase precursor:threonine deaminase] [gn:ilv1] [gtcf:2.8:5.3:6.6] [ec:4.2.1.16] [keggfc:5.3] [sgdfc:1.1:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5806	38877_f3_16	3592	17695	1245	415	YER141W	1031	3.2(10)-104	Saccharomyces cerevisiae	[ui:yer141w] [pn:cytochrome oxidase assembly factor:cytochrome c oxidase assembly protein] [gn:cox15] [gtcf:2.8:12.16] [keggfc:14.2] [sgdfc:6.4.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1344	3906275_fl_1	3593	17696	909	303	YER154W	478	1.3(10)-45	Saccharomyces cerevisiae	[ui:yer154w] [pn:cytochrome oxidase biogenesis protein:cytochrome oxidase biogenesis protein oxal precursor] [gn:oxal:pet1402] [gtcf:2.8:12.16] [keggfc:14.2] [sgdfc:2.5.0:6.4.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3807	24484452_c1_7	3594	17697	1644	548	YER168C	927	3.5(10)-93	Saccharomyces cerevisiae	[ui:yer168c] [pn:tma nucleotidyltransferase:tma nucleotidyltransferase precursor:tma adenyllyltransferase:tma cca-pyrophosphorylase] [gn:cca:tnt1] [gtcf:2.8:10.1:10.2:10.6:14.1] [ec:2.7.7.25] [keggfc:14.1] [sgdfc:4.6.0:9.2.0:9.5]

CONTIG4129	3223908_c3_14	3595	17698	588	196	YER170W	501	4.7(10)-48	Saccharomyces cerevisiae	[ui:yer170w] [pn:adenylate kinase, mitochondrial:adenylate kinase] [gn:adk2:pak3] [gtcf:2.8.4.1:12.13:12.8] [ec:2.7.4.3] [keggfc:4.1] [sgdgc:1.3.8.3.1.0.9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4374	6347656_f2_1	3596	17699	2058	686	YFL036W	1308	1.5(10)-133	Saccharomyces cerevisiae	[ui:yfl036w] [pn:dna-directed rna polymerase, mitochondrial:dna-directed rna polymerase] [gn:rpo41] [gtcf:2.8.4.1:4.2:10.2:10.8] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdgc:3.6.0.4.8.1.9.7.0] [db:gtc-saccharomyces ce]
CONTIG4904	19744788_c2_4	3597	17700	1014	338	YFL036W	748	3.2(10)-73	Saccharomyces cerevisiae	[ui:yfl036w] [pn:dna-directed rna polymerase, mitochondrial:dna-directed rna polymerase] [gn:rpo41] [gtcf:2.8.4.1:4.2:10.2:10.8] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdgc:3.6.0.4.8.1.9.7.0] [db:gtc-saccharomyces ce]

CONTIG5682	35347688_c3_27	3598	17701	834	278	YFL036W	392	4.2(10)-35	Saccharomyces cerevisiae	[ui:yfl036w] [pn:dna-directed rna polymerase, mitochondrial:dna-directed rna polymerase mitochondrial precursor] [gn:rpo41] [gtcf:2.8.4.1.4.2:10.2:10.8] [ec:2.7.7.6] [keggfc:4.1.4.2] [sgdfc:3.6.0.4.8.1.9.7.0] [db:gtc-saccharomyces ce]
CONTIG5682	2113792_c2_25	3599	17702	2190	730	YFL036W	189	8.4(10)-11	Saccharomyces cerevisiae	[ui:yfl036w] [pn:dna-directed rna polymerase, mitochondrial:dna-directed rna polymerase mitochondrial precursor] [gn:rpo41] [gtcf:2.8.4.1.4.2:10.2:10.8] [ec:2.7.7.6] [keggfc:4.1.4.2] [sgdfc:3.6.0.4.8.1.9.7.0] [db:gtc-saccharomyces ce]
CONTIG1885	34406587_f2_1	3600	17703	720	240	YFL016C	268	4.7(10)-36	Saccharomyces cerevisiae	[ui:yfl016c] [pn:heat shock protein - chaperone:protein precursor] [gn:mdj1] [gtcf:12.7.2.8.10.5:10.7:13.2] [keggfc:14.2] [sgdfc:6.1.0.9.7.0:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5665	13862575_f1_1	3601	17704	267	89	YFR049W	98	2.5(10)-5	Saccharomyces cerevisiae	[ui:yfr049w] [pn:ribosomal protein, mitochondrial:mitochondrial 40s ribosomal protein ymr-31 precursor] [gn:ymr31] [gtcf:2.8.10.4] [keggfc:14.2] [sgdfc:5.1.0.9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5123	977140_c2_10	3602	17705	1860	620	YGL119W	1345	1.8(10)-137	Saccharomyces cerevisiae	[ui:ygl119w] [pn:ubiquinol cytochrome-c reductase complex assembly protein:protein precursor] [gn:abc1] [gtfc:2.8:12.16] [keggfc:14.2] [sgdgc:2.5:0.6:4.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5275	10574224_c1_14	3603	17706	219	73	YGL068W	229	3.2(10)-19	Saccharomyces cerevisiae	[ui:ygl068w] [pn:probable ribosomal protein 112:putative mitochondrial 60s ribosomal protein 17/112 precursor] [gtfc:2.8:10.4] [keggfc:14.2] [sgdgc:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5447	24407830_f1_3	3604	17707	543	181	YGR076C	233	1.2(10)-19	Saccharomyces cerevisiae	[ui:ygr076c] [pn:ribosomal protein ymr26:yml25, mitochondrial:mitochondrial 60s ribosomal protein 125:yml25] [gn:mrp125:ymr26] [gtfc:2.8:10.4] [keggfc:14.2] [sgdgc:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1387	19573387_c1_2	3605	17708	945	315	YGR094W	952	7.7(10)-96	Saccharomyces cerevisiae	[ui:ygr094w] [pn:valyl-tRNA synthetase:valyl-tRNA synthetase, mitochondrial precursor:valine-tRNA ligase:valrs] [gn:vas1] [gtfc:2.8:5.7:10.6] [ec:6.1.1.9] [keggfc:5.7:10.1:10.2] [sgdgc:5.4:0.9:2.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3315	3157502_f2_2	3606	17709	1284	428	YGR094W	1122	7.5(10)-114	Saccharomyces cerevisiae	[ui:YGR094w] [pn:valyl-tRNA synthetase:valyl-tRNA synthetase, mitochondrial precursor:valine--tRNA ligase:valrs] [gn:vas1] [gtcf:2.8:5.7:10.6] [ec:6.1.1.9] [keggf:5.7:10.1:10.2] [sgdfc:5.4:0.9:2.0:9.7.0] [db:gtc-saccharomyces cerevi
CONTIG3315	4102157_f1_1	3607	17710	1155	385	YGR094W	1601	1.3(10)-164	Saccharomyces cerevisiae	[ui:YGR094w] [pn:valyl-tRNA synthetase:valyl-tRNA synthetase, mitochondrial precursor:valine--tRNA ligase:valrs] [gn:vas1] [gtcf:2.8:5.7:10.6] [ec:6.1.1.9] [keggf:5.7:10.1:10.2] [sgdfc:5.4:0.9:2.0:9.7.0] [db:gtc-saccharomyces cerevi
CONTIG5713	13773450_f1_1	3608	17711	486	162	YGR171C	180	5.0(10)-13	Saccharomyces cerevisiae	[ui:YGR171c] [pn:methionyl-tRNA synthetase:methionyl-tRNA synthetase, mitochondrial:methionine--tRNA ligase:metrs] [gn:msm1] [gtcf:2.8:5.4:6.4:10.6] [ec:6.1.1.10] [keggf:5.4:6.4:10.1:10.2] [sgdfc:5.4:0.9:7.0] [db:gtc-saccharomyces c
CONTIG3802	4335052_f2_3	3609	17712	444	148	YGR174C	331	5.0(10)-30	Saccharomyces cerevisiae	[ui:YGR174c] [pn:ubiquinol-cytochrome c reductase assembly factor:protein precursor] [gn:cbp4] [gtcf:2.8:12.16] [keggf:14.2] [sgdfc:2.5:0.6:4.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

b2x13522.y	23632941_c3_2	3610	17713	618	206	YGR207C	437	2.8(10)-41	Saccharomyces cerevisiae	[ui:ygr207c] [pn:electron-transferring flavoprotein, beta chain:probable electron transfer flavoprotein beta-subunit:beta- etf] [gn:etf-beta:g7742] [gtcf:2.8] [keggf:14.2] [sgdfc:2.5.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
b2x14802.y	16413507_c1_1	3611	17714	528	176	YGR207C	349	6.2(10)-32	Saccharomyces cerevisiae	[ui:ygr207c] [pn:electron-transferring flavoprotein, beta chain:probable electron transfer flavoprotein beta-subunit:beta- etf] [gn:etf-beta:g7742] [gtcf:2.8] [keggf:14.2] [sgdfc:2.5.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2016	787562_f3_1	3612	17715	702	234	YGR220C	396	6.5(10)-37	Saccharomyces cerevisiae	[ui:ygr220c] [pn:ribosomal protein of the large subunit, mitochondrial:mitochondrial 60s ribosomal protein 19 precursor:ym19] [gn:mrp19:g8520] [gtcf:2.8:10.4] [keggf:14.2] [sgdfc:5.1.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2325	34267142_f1_1	3613	17716	522	174	YHL004W	322	4.5(10)-29	Saccharomyces cerevisiae	[ui:yhl004w] [pn:ribosomal protein of the small subunit, mitochondrial:mitochondrial 40s ribosomal protein] [gn:mrp4] [gtcf:2.8:10.4] [keggf:14.2] [sgdfc:5.1.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2859	30595705_c2_5	3614	17717	885	295	YHL004W	146	3.0(10)-8	Saccharomyces cerevisiae	[ui:yhl004w] [pn:ribosomal protein of the small subunit, mitochondrial:mitochondrial 40s ribosomal protein] [gn:mrp4] [gicf:2.8:10.4] [keggf:14.2] [sgdfc:5.1.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2395	1210300_c3_6	3615	17718	687	229	YHR008C	691	3.6(10)-68	Saccharomyces cerevisiae	[ui:yhr008c] [pn:superoxide dismutase:mn precursor, mitochondrial:superoxide dismutase precursor:mn] [gn:sod2] [gicf:2.8:12.12] [ec:1.15.1.1] [keggf:14.1] [sgdfc:9.7.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4301	15660212_f2_4	3616	17719	204	68	YHR008C	91	0.00044	Saccharomyces cerevisiae	[ui:yhr008c] [pn:superoxide dismutase:mn precursor, mitochondrial:superoxide dismutase precursor:mn] [gn:sod2] [gicf:2.8:12.12] [ec:1.15.1.1] [keggf:14.1] [sgdfc:9.7.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4301	15673286_f2_5	3617	17720	516	172	YHR008C	578	3.3(10)-56	Saccharomyces cerevisiae	[ui:yhr008c] [pn:superoxide dismutase:mn precursor, mitochondrial:superoxide dismutase precursor:mn] [gn:sod2] [gicf:2.8:12.12] [ec:1.15.1.1] [keggf:14.1] [sgdfc:9.7.0:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5325	4335003_c2_13	3618	17721	543	181	YHR024C	310	1.5(10)-27	Saccharomyces cerevisiae	[ui:yhr024c] [pn:processing peptidase, catalytic 53kda:alpha subunit, mitochondrial:mitochondrial processing peptidase alpha subunit precursor:alpha-mpp] [gn:mas2:mif2] [gtcf:2.8:10.7] [ec:3.4.24.64] [keggfc:14.1] [sgdfc:6.3.0:9.7.0]
CONTIG5325	14455305_c1_7	3619	17722	1137	379	YHR024C	817	1.6(10)-81	Saccharomyces cerevisiae	[ui:yhr024c] [pn:processing peptidase, catalytic 53kda:alpha subunit, mitochondrial:mitochondrial processing peptidase alpha subunit precursor:alpha-mpp] [gn:mas2:mif2] [gtcf:2.8:10.7] [ec:3.4.24.64] [keggfc:14.1] [sgdfc:6.3.0:9.7.0]
CONTIG2505	20490811_fl_1	3620	17723	1257	419	YHR037W	1216	8.3(10)-124	Saccharomyces cerevisiae	[ui:yhr037w] [pn:l-pyrroline-5-carboxylate dehydrogenase:delta-l-pyrroline-5-carboxylate dehydrogenase precursor:p5c dehydrogenase] [gn:put2] [gtcf:2.8:5.1:5.10:6.6] [ec:1.5.1.12] [keggfc:5.1:5.10] [sgdfc:1.1:1:9.7.0] [db:gtc-sacchar
CONTIG1990	819687_f2_2	3621	17724	1170	390	YHR120W	542	1.5(10)-51	Saccharomyces cerevisiae	[ui:yhr120w] [pn:dna mismatch repair protein, mitochondrial:muts protein homolog 1] [gn:msh1] [gtcf:2.8:10.8] [keggfc:14.2] [sgdfc:3.7.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3662	30270253_c2_7	3622	17725	264	88	YHR120W	179	1.3(10)-12	Saccharomyces cerevisiae	[ui:yhr120w] [pn:dna mismatch repair protein, mitochondrial:mut protein homolog 1] [gn:msh1] [gtcf:2.8:10.8] [keggf:14.2] [sgdfc:3.7:0.9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2483	2506556_c1_3	3623	17726	717	239	YHR147C	437	2.8(10)-41	Saccharomyces cerevisiae	[ui:yhr147c] [pn:ribosomal protein of the large subunit, mitochondrial:mitochondrial 60s ribosomal protein l6 precursor:ym16] [gn:mrp16] [gtcf:2.8:10.4] [keggf:14.2] [sgdfc:5.1:0.9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2293	40636_c1_3	3624	17727	972	324	YIL043C	587	3.7(10)-57	Saccharomyces cerevisiae	[ui:yil043c] [pn:cytochrome-b5 reductase:putative nadh-cytochrome b5 reductase:p35] [gn:cbr1:cbr5:cbr] [gtcf:2.8:7.1] [ec:1.6.2.2] [keggf:4.4] [sgdfc:2.5:0.9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG624	20899163_f2_2	3625	17728	342	114	YJL208C	330	6.4(10)-30	Saccharomyces cerevisiae	[ui:yjl208c] [pn:nuclease, mitochondrial:mitochondrial nuclease] [gn:nuc1:j0310:hre329] [gtcf:2.8:4.4:10.10] [ec:3.1.30.-] [keggf:14.1] [sgdfc:1.3.6:9.7.0] [db:gtc-saccharomyces cerevisiae]
b3x14607.y	23866630_c3_2	3626	17729	519	173	YJL208C	559	3.5(10)-54	Saccharomyces cerevisiae	[ui:yjl208c] [pn:nuclease, mitochondrial:mitochondrial nuclease] [gn:nuc1:j0310:hre329] [gtcf:2.8:4.4:10.10] [ec:3.1.30.-] [keggf:14.1] [sgdfc:1.3.6:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1101	24476527_c1_2	3627	17730	594	198	YJL180C	287	2.2(10)-25	Saccharomyces cerevisiae	[ui:yjl180c] [pn:fl0-atpase complex assembly protein:atp12 protein precursor] [gn:atp12:j0486] [gtcf:2.8:12.16] [keggf:14.2] [sgdf:6.4:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4516	4017160_c1_9	3628	17731	951	317	YJL133W	442	8.6(10)-42	Saccharomyces cerevisiae	[ui:yjl133w] [pn:rna splicing protein and member of the mitochondrial carrier family:mcf:mitochondrial rna splicing protein mrs3] [gn:mrs3:j0675] [gtcf:2.8:10.2] [keggf:14.2] [sgdf:4.9:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5288	4322777_c2_15	3629	17732	2220	740	YJL102W	1303	5.0(10)-133	Saccharomyces cerevisiae	[ui:yjl102w] [pn:translation elongation factor, mitochondrial:elongation factor g, mitochondrial 2 precursor:mef-g-2] [gn:mef2:j0826] [gtcf:2.8:10.7] [keggf:14.2] [sgdf:5.2:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5801	781312_c1_25	3630	17733	843	281	YJL063C	175	2.1(10)-13	Saccharomyces cerevisiae	[ui:yjl063c] [pn:ribosomal protein l17, mitochondrial:mitochondrial 60s ribosomal protein l8:ym18] [gn:mrp18:j1125:hrd238] [gtcf:2.8:10.4] [keggf:14.2] [sgdf:5.1:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3687	19609687_fl_1	3631	17734	1806	602	YJR016C	2114	5.7(10)-219	Saccharomyces cerevisiae	[ui:yjr016c] [pn:dihydroxy-acid dehydratase: dihydroxy-acid dehydratase precursor: dad:2,3-dihydroxy acid hydrolyase] [gn:ilv3:j1450] [gtcf:2.8:5.7:6.6:9.5] [ec:4.2.1.9] [keggf:5.7:9.5] [sgdfc:1.1:1:9.7.0] [db:gtc-saccharomyces cerev
CONTIG5200	23674202_c1_10	3632	17735	1965	655	YJR045C	1663	3.6(10)-171	Saccharomyces cerevisiae	[ui:yjr045c] [pn:mitochondrial heat shock protein 70-related protein: mitochondrial heat shock protein ssc1 precursor: endonuclease ssc1 75 kd subunit] [gn:ssc1:ens1:j1639] [gtcf:12.7:2.8:10.2:10.5:10.7:13.2] [keggf:14.2] [sgdfc:4.9.0]
CONTIG5304	36204187_c3_9	3633	17736	1551	517	YJR045C	1998	1.1(10)-206	Saccharomyces cerevisiae	[ui:yjr045c] [pn:mitochondrial heat shock protein 70-related protein: mitochondrial heat shock protein ssc1 precursor: endonuclease ssc1 75 kd subunit] [gn:ssc1:ens1:j1639] [gtcf:12.7:2.8:10.2:10.5:10.7:13.2] [keggf:14.2] [sgdfc:4.9.0]
CONTIG4485	4689000_fl_2	3634	17737	363	121	YJR048W	479	1.0(10)-45	Saccharomyces cerevisiae	[ui:yjr048w] [pn:cytochrome c isoform 1: cytochrome c, iso-1] [gn:cyc1:j1653] [gtcf:2.8] [keggf:14.2] [sgdfc:2.5:0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4669	3940677_c3_10	3635	17738	921	307	YJR095W	956	3.0(10)-96	Saccharomyces cerevisiae	[ui:yjr095w] [pn:regulator of acetyl-coa synthetase activity] [gn:acr1:j1921] [gtcf:2.8:12.13] [keggf:14.2] [sgdfc:1.5:2:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5093	312_f2_2	3636	17739	813	271	YJR113C	458	1.7(10)-43	Saccharomyces cerevisiae	[ui:yjr113c] [pn:similarity to bacterial, chloroplast and mitochondrial ribosomal protein s7:putative 40s ribosomal protein yjr113c] [gn:j2020] [gtcf:2.8:10.4] [keggf:14.2] [sgdf:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3874	15658430_c3_10	3637	17740	774	258	YJR144W	566	6.2(10)-55	Saccharomyces cerevisiae	[ui:yjr144w] [pn:mitochondrial genome maintenance protein:mitochondrial genome maintenance protein mgm101 precursor] [gn:mgm101:mgm9:j2181] [gtcf:2.8] [keggf:14.2] [sgdf:9.7.0] [db:gtc-saccharomyces cerevisiae]
blx12579.y	36500900_c1_2	3638	17741	561	187	YKL194C	463	5.2(10)-44	Saccharomyces cerevisiae	[ui:ykl194c] [pn:threonine--trna ligase, mitochondrial:threonyl-trna synthetase, mitochondrial precursor:threonine--trna ligase:thrs] [gn:mst1] [gtcf:2.8:5.3:10.6] [ec:6.1.1.3] [keggf:5.3:10.1:10.2] [sgdf:5.4:0.9:7.0] [db:gtc-sacc
CONTIG5757	178936_f1_1	3639	17742	984	328	YKL150W	835	2.0(10)-83	Saccharomyces cerevisiae	[ui:ykl150w] [pn:cytochrome-b5 reductase:nadh-cytochrome b5 reductase precursor:p34 / p32] [gn:mcr1:ykl605] [gtcf:2.8:7.1] [ec:1.6.2.2] [keggf:4.4] [sgdf:2.5:0.9:7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1385	24870933_c1_5	3640	17743	612	204	YKL142W	202	2.2(10)-16	Saccharomyces cerevisiae	[ui:ykl142w] [pn:ribosomal protein, mitochondrial:mitochondrial 40s ribosomal protein mrp8] [gn:mrp8:ykl13] [gtcf:2.8:10.4] [keggf:14.2] [sgdf:5.1.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5410	12615636_c3_18	3641	17744	1800	600	YKL134C	1115	4.2(10)-113	Saccharomyces cerevisiae	[ui:ykl134c] [pn:mitochondrial intermediate peptidase:hypothetical zinc metalloproteinase ykl134c] [gtcf:10.7:2.8] [ec:3.4.24.-] [keggf:14.1] [sgdf:6.3.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5780	5094437_f2_21	3642	17745	519	173	YKL134C	237	6.2(10)-19	Saccharomyces cerevisiae	[ui:ykl134c] [pn:mitochondrial intermediate peptidase:hypothetical zinc metalloproteinase ykl134c] [gtcf:10.7:2.8] [ec:3.4.24.-] [keggf:14.1] [sgdf:6.3.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5465	15017827_f3_4	3643	17746	1053	351	YKL120W	909	2.7(10)-91	Saccharomyces cerevisiae	[ui:ykl120w] [pn:similarity to mitochondrial uncoupling proteins:mcf:mitochondrial carrier protein pmt] [gn:pmt:pmt1:ykl522] [gtcf:2.8] [keggf:14.2] [sgdf:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3351	1188257_f3_3	3644	17747	795	265	YKL087C	501	4.7(10)-48	Saccharomyces cerevisiae	[ui:ykl087c] [pn:holocytochrome-c1 synthase:cytochrome c1 heme lyase:cc1hl] [gn:cyt2] [gtcf:2.8:9.12:10.7] [ec:4.4.1.-] [keggf:14.1] [sgdf:1.7.2:6.3.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3460	14625285_f3_3	3645	17748	1116	372	YKR066C	728	4.2(10)-72	Saccharomyces cerevisiae	[ui:ykr066c] [pn:cytochrome-c peroxidase precursor:ccp] [gn:ccp1:ccp:cpo] [gtcf:2.8:12.12] [ec:1.11.1.5] [keggf:14.1] [sgdf:9.7.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5793	35189387_c2_20	3646	17749	936	312	YKR066C	550	3.1(10)-53	Saccharomyces cerevisiae	[ui:ykr066c] [pn:cytochrome-c peroxidase precursor:ccp] [gn:ccp1:ccp:cpo] [gtcf:2.8:12.12] [ec:1.11.1.5] [keggf:14.1] [sgdf:9.7.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG859	26257692_c3_1	3647	17750	921	307	YLR067C	127	6.0(10)-5	Saccharomyces cerevisiae	[ui:ykr067c] [pn:required for stability and translation of cox1 mma:pet309:12189] [gn:pet309:12189] [gtcf:2.8:10.2:10.7] [keggf:14.2] [sgdf:4.12.0:5.3.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2753	167508_c3_5	3648	17751	804	268	YLR069C	768	2.5(10)-76	Saccharomyces cerevisiae	[ui:ykr069c] [pn:translation elongation factor g, mitochondrial:elongation factor g, mitochondrial l precursor:mef-g-1] [gn:mef1] [gtcf:2.8:10.7] [keggf:14.2] [sgdf:5.2.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
b3x14382.x	34428141_c2_2	3649	17752	630	210	YLR069C	765	5.0(10)-76	Saccharomyces cerevisiae	[ui:ykr069c] [pn:translation elongation factor g, mitochondrial:elongation factor g, mitochondrial l precursor:mef-g-1] [gn:mef1] [gtcf:2.8:10.7] [keggf:14.2] [sgdf:5.2.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4884	23945307_f3_2	3650	17753	2271	757	YLR139C	136	1.3(10)-5	Saccharomyces cerevisiae	[ui:ylr139c] [pn:suppresses lethality of ssm4 deletion:sis1 protein] [gn:sis1:i3162] [gtcf:2.8:10.2] [keggc:14.2] [sgdfc:4.12.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2451	24298302_f1_1	3651	17754	1446	482	YLR142W	1009	7.0(10)-102	Saccharomyces cerevisiae	[ui:ylr142w] [pn:proline oxidase:proline oxidase precursor] [gn:put1:i3170:i9606] [gtcf:2.8:5.3:6.6] [ec:1.5.3.-] [keggc:14.1] [sgdfc:1.1:1.1.4.9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4430	9853302_f1_1	3652	17755	1449	483	YLR163C	1248	3.3(10)-127	Saccharomyces cerevisiae	[ui:ylr163c] [pn:mitochondrial processing peptidase:mitochondrial processing peptidase beta subunit precursor:beta-mpp:pep] [gn:mas1:mif1:i9632] [gtcf:2.8:10.7] [ec:3.4.24.64] [keggc:14.1] [sgdfc:6.3.0:9.7.0] [db:gtc-saccharomyces c
CONTIG692	4898961_c3_3	3653	17756	468	156	YLR168C	368	6.0(10)-34	Saccharomyces cerevisiae	[ui:ylr168c] [pn:probably involved in intramitochondrial protein sorting:msf1 protein] [gtcf:2.8:10.7:1.1] [keggc:14.2] [sgdfc:6.2.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2059	42707_c3_5	3654	17757	240	80	YLR203C	119	1.2(10)-6	Saccharomyces cerevisiae	[ui:ylr203c] [pn:possibly involved in translational activation of cox1 and cob mrna:mss51 protein] [gn:mss51:i8167] [gtcf:2.8:10.7] [keggc:14.2] [sgdfc:5.3.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3403	23867908_c1_7	3655	17758	300	100	YLR203C	124	3.5(10)-7	Saccharomyces cerevisiae	[ui:ylr203c] [pn:possibly involved in translational activation of cox1 and cob mma:mss51 protein] [gn:mss51:18167] [gtcf:2.8:10.7] [keggf:14.2] [sgdf:5.3.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3403	19000_c1_6	3656	17759	672	224	YLR203C	620	1.2(10)-60	Saccharomyces cerevisiae	[ui:ylr203c] [pn:possibly involved in translational activation of cox1 and cob mma:mss51 protein] [gn:mss51:18167] [gtcf:2.8:10.7] [keggf:14.2] [sgdf:5.3.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
b9x10g13.y	4898505_c2_2	3657	17760	567	189	YLR259C	798	1.6(10)-79	Saccharomyces cerevisiae	[ui:ylr259c] [pn:heat shock protein-chaperone, mitochondrial:heat shock protein 60 precursor:stimulator factor i 66 kd component:p66:cpn60] [gn:hsp60:mif4:18479] [gtcf:12.7.2.8:10.5:10.7:13.2] [keggf:14.2] [sgdf:6.1.0:9.7.0:11.1.
CONTIG3815	13711563_f2_2	3658	17761	834	278	YLR355C	920	1.8(10)-92	Saccharomyces cerevisiae	[ui:ylr355c] [pn:keto-l-acid reductoisomerase:keto-l-acid reductoisomerase precursor:aceto-hydroxy-acid reductoisomerase:alpha-keto-beta-hydroxylacil reductoisomerase] [gn:ilv5:19638] [gtcf:2.8:5.7:6.6:9.5] [ec:1.1.1.86] [keggf:5.7:9.

CONTIG5098	14144091_f2_3	3659	17762	210	70	YLR355C	271	1.1(10)-23	Saccharomyces cerevisiae	[ui:ylr355c] [pn:keto]-acid reductoisomerase:keto]-acid reductoisomerase precursor:aceto-hydroxy-acid reductoisomerase:alpha-keto-beta-hydroxylacil reductoisomerase] [gn:ilv5:19638] [gtcf:2.8:5.7:6.9:5] [ec:1.1.1.86] [keggfc:5.7:9.
CONTIG131	33784438_c1_3	3660	17763	510	170	YLR382C	170	1.1(10)-11	Saccharomyces cerevisiae	[ui:ylr382c] [pn:leucine--trna ligase precursor, mitochondrial:leucyl-trna synthetase, mitochondrial precursor:leucine--trna ligase:leurs] [gn:nam2:msl1:13502] [gtcf:2.8:5.7:10.2:10.6] [ec:6.1.1.4] [keggfc:5.7:10.1:10.2] [sgdfc:4.9.0
CONTIG4375	22459702_f3_6	3661	17764	372	124	YLR382C	236	1.0(10)-18	Saccharomyces cerevisiae	[ui:ylr382c] [pn:leucine--trna ligase precursor, mitochondrial:leucyl-trna synthetase, mitochondrial precursor:leucine--trna ligase:leurs] [gn:nam2:msl1:13502] [gtcf:2.8:5.7:10.2:10.6] [ec:6.1.1.4] [keggfc:5.7:10.1:10.2] [sgdfc:4.9.0

CONTIG3253	16689694_c2_5	3662	17765	1515	505	YLR382C	1341	4.7(10)-137	Saccharomyces cerevisiae	[ui:ylr382c] [pn:leucine--trna ligase precursor, mitochondrial:leucyl-trna synthetase, mitochondrial precursor:leucine--trna ligase:leurs] [gn:nam2:msl1:13502] [gtcf:2.8:5.7:10.2:10.6] [ec:6.1.1.4] [keggc:5.7:10.1:10.2] [sgdfc:4.9.0]
CONTIG4120	26195187_f3_5	3663	17766	621	207	YLR393W	324	2.7(10)-29	Saccharomyces cerevisiae	[ui:ylr393w] [pn:f1f0 atpase complex assembly protein:protein] [gn:atp10] [gtcf:2.8:12.16] [keggc:14.2] [sgdfc:6.4.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3359	1178567_f3_3	3664	17767	513	171	YLR439W	153	1.2(10)-10	Saccharomyces cerevisiae	[ui:ylr439w] [pn:ribosomal protein, mitochondrial:mitochondrial 60s ribosomal protein 14 precursor:ym14] [gn:mrp14:l9753] [gtcf:2.8:10.4] [keggc:14.2] [sgdfc:5.1.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3871	24814713_c1_8	3665	17768	675	225	YML078W	549	4.0(10)-53	Saccharomyces cerevisiae	[ui:ym1078w] [pn:cyclophilin:peptidylprolyl isomerase, mitochondrial:peptidyl-prolyl cis-trans isomerase c precursor:ppiase:rotamase:cyclophilin c:ppi-iii] [gn:cpr3:cyp3] [gtcf:2.8:10.5:10.7:12.7] [ec:5.2.1.8] [keggc:14.1] [sgdfc:6.6]

CONTIG5562	4334651_c3_13	3666	17769	846	282	YML025C	396	6.5(10)-37	Saccharomyces cerevisiae	[ui:ym1025c] [pn:ribosomal protein, mitochondrial:putative 14p like ribosomal protein] [gtcf:2.8:10.4] [keggf:14.2] [sgdfc:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5744	2400410_c2_22	3667	17770	645	215	YML021C	472	5.7(10)-45	Saccharomyces cerevisiae	[ui:ym1021c] [pn:uracil-dna glycosylase:uracil-dna glycosylase precursor] [gn:ung1] [gtcf:2.8:10.1:10.2:10.8:14.1] [ec:3.2.2.-] [keggf:14.1] [sgdfc:3.7:0.9:5.0:9.7:0] [db:gtc-saccharomyces cerevisiae]
CONTIG1523	24616002_c3_3	3668	17771	405	135	YMR023C	283	2.6(10)-24	Saccharomyces cerevisiae	[ui:ymr023c] [pn:mitochondrial gipase involved in expression of cox1:mitochondrial gtpase mss1 precursor] [gn:mss1:pet53:ym9711] [gtcf:2.8:10.2:10.7] [keggf:14.2] [sgdfc:4.9:0.5:2.0:9.7:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3233	5094182_f3_3	3669	17772	1227	409	YMR023C	700	4.0(10)-69	Saccharomyces cerevisiae	[ui:ymr023c] [pn:mitochondrial gipase involved in expression of cox1:mitochondrial gtpase mss1 precursor] [gn:mss1:pet53:ym9711] [gtcf:2.8:10.2:10.7] [keggf:14.2] [sgdfc:4.9:0.5:2.0:9.7:0] [db:gtc-saccharomyces cerevisiae]

CONTIG5743	29923130_f2_9	3670	17773	1266	422	YMR024W	449	1.6(10)-42	Saccharomyces cerevisiae	[ui:ymr024w] [pn:ribosomal protein of the large subunit, mitochondrial:mitochondrial 60s ribosomal protein l3 precursor:yml3] [gn:mrp13:ym9711] [gtcf:2.8:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5040	4729557_c3_15	3671	17774	498	166	YMR035W	450	1.2(10)-42	Saccharomyces cerevisiae	[ui:ymr035w] [pn:mitochondrial inner membrane protease subunit:mitochondrial inner membrane protease subunit 2] [gn:imp2:ym9973] [gtcf:2.8:10.11:10.7:11.1] [ec:3.4.99.-] [keggfc:14.1] [sgdfc:6.2.0:6.3.0:9.7.0:11.2.1] [db:gtc-saccharo]
CONTIG5507	4725027_f3_6	3672	17775	774	258	YMR038C	420	1.8(10)-39	Saccharomyces cerevisiae	[ui:ymr038c] [pn:regulation of lysine biosynthesis:homocitrate dehydratase] [gn:lys7:ym9532] [gtcf:5.8:1.2:2.8] [ec:4.2.-.-] [keggfc:14.1] [sgdfc:1.4.1:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2077	26345250_f2_1	3673	17776	1155	385	YMR089C	1539	4.9(10)-158	Saccharomyces cerevisiae	[ui:ymr089c] [pn:protease of the sec18/cdc48/pas1 family of atpases:aaa:mitochondrial respiratory chain complexes assembly protein real:tat-binding homolog 12] [gn:rcal:yal2:ym9582] [gtcf:2.8:10.11:12.16] [ec:3.4.24.-] [keggfc:14.1]

CONTIG3564	29335008_f2_2	3674	17777	315	105	YMR089C	273	9.5(10)-23	Saccharomyces cerevisiae	[ui:ymr089c] [pn:protease of the sec18/cdc48/pas1 family of atpases:aaa:mitochondrial respiratory chain complexes assembly protein real:tat-binding homolog 12] [gn:rcal:yta12:ym9582] [gtcf:2.8:10.11:12.16] [ec:3.4.24.-] [keggf:14.1]
CONTIG1243	900305_f3_2	3675	17778	555	185	YMR150C	538	5.7(10)-52	Saccharomyces cerevisiae	[ui:ymr150c] [pn:protease, mitochondrial:mitochondrial inner membrane protease subunit 1] [gn:imp1:pet2858:ym9375] [gtcf:2.8:10.11:11.1] [ec:3.4.99.-] [keggf:14.1] [sgdf:6.2.0:6.3.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5578	21879093_f1_1	3676	17779	3006	1002	YMR189W	3211	0	Saccharomyces cerevisiae	[ui:ymr189w] [pn:glycine decarboxylase subunit:glycine dehydrogenase:decarboxylating precursor:glycine decarboxylase:glycine cleavage system p- protein] [gn:gcv2:gsd2:ym9646] [gtcf:2.8:5.3] [ec:1.4.4.2] [keggf:5.3] [sgdf:1.1.4:9.7.
CONTIG2692	36515911_c2_5	3677	17780	474	158	YMR193W	172	3.5(10)-13	Saccharomyces cerevisiae	[ui:ymr193w] [pn:ribosomal protein of the large subunit, mitochondrial:mitochondrial 60s ribosomal protein l24 precursor:ymi24] [gn:mrp124:ym9646] [gtcf:2.8:10.4] [keggf:14.2] [sgdf:5.1.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4790	24416057_f2_4	3678	17781	375	125	YMR225C	186	1.2(10)-14	Saccharomyces cerevisiae	[lui:ymr225c] [pn:ribosomal protein ymr44, mitochondrial:mitochondrial 60s ribosomal protein l44:yml44] [gn:mrpl44:ymr44:ym9959] [gtcf:2.8:10.4] [keggf:14.2] [sgdf:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1699	33672643_f1_1	3679	17782	579	193	YMR228W	213	2.5(10)-17	Saccharomyces cerevisiae	[lui:ymr228w] [pn:rna polymerase specific factor, mitochondrial:mitochondrial replication protein mtf1:rf1023:mitochondrial specificity factor] [gn:mtf1:ym9959] [gtcf:2.8:10.2:10.8] [keggf:14.2] [sgdf:3.7:0.4:8.1:9.7.0] [db:gtc-sacc]
CONTIG5740	79526_c1_13	3680	17783	912	304	YMR244W	761	1.3(10)-75	Saccharomyces cerevisiae	[lui:ymr244w] [pn:similarity to nca3 and sun4 protein] [gtcf:2.8] [keggf:14.2] [sgdf:2.5:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3274	35947500_f3_2	3681	17784	204	68	YMR286W	96	4.0(10)-5	Saccharomyces cerevisiae	[lui:ymr286w] [pn:ribosomal protein of the large subunit, mitochondrial:mitochondrial 60s ribosomal protein l33:yml33] [gn:mrpl33:ym8021] [gtcf:2.8:10.4] [keggf:14.2] [sgdf:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5730	12772760_f3_8	3682	17785	1911	637	YMR287C	132	9.1(10)-9	Saccharomyces cerevisiae	[ui:ymr287c] [pn:3"-5" exonuclease for rna 3" ss-tail, mitochondrial:mitochondrial biogenesis msu1 protein] [gn:msu1:ym8021] [gtcf:2.8:4.4:10.10] [keggf:14.2] [sgdf:1.3:6.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5730	4017186_f3_9	3683	17786	1575	525	YMR287C	176	1.0(10)-20	Saccharomyces cerevisiae	[ui:ymr287c] [pn:3"-5" exonuclease for rna 3" ss-tail, mitochondrial:mitochondrial biogenesis msu1 protein] [gn:msu1:ym8021] [gtcf:2.8:4.4:10.10] [keggf:14.2] [sgdf:1.3:6.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5419	20078556_f2_3	3684	17787	2124	708	YMR302C	557	2.7(10)-117	Saccharomyces cerevisiae	[ui:ymr302c] [pn:involved in early maturation of pre-rna:ma12 protein] [gn:ma12:prp12:ym9952] [gtcf:2.8:10.3] [keggf:14.2] [sgdf:4.3:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5419	2236262_f3_8	3685	17788	459	153	YMR302C	113	1.3(10)-5	Saccharomyces cerevisiae	[ui:ymr302c] [pn:involved in early maturation of pre-rna:ma12 protein] [gn:ma12:prp12:ym9952] [gtcf:2.8:10.3] [keggf:14.2] [sgdf:4.3:0.9:7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG557	22273311_c3_2	3686	17789	783	261	YNL315C	448	2.0(10)-42	Saccharomyces cerevisiae	[ui:ynl315c] [pn:fl0-atpase complex assembly protein:atp11 protein precursor] [gn:atp11:n0357] [gtcf:2.8:12.16] [keggf:14.2] [sgdfc:6.4:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5405	13945135_c3_9	3687	17790	870	290	YNL252C	527	8.5(10)-51	Saccharomyces cerevisiae	[ui:ynl252c] [pn:ribosomal protein yml130, mitochondrial:mitochondrial 60s ribosomal protein l30 precursor:ym130] [gn:mrp130:n0864] [gtcf:2.8:10.4] [keggf:14.2] [sgdfc:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2737	14531262_c2_4	3688	17791	1641	547	YNL237W	758	2.2(10)-90	Saccharomyces cerevisiae	[ui:ynl237w] [pn:weak similarity to mitochondrial electron transport proteins:atp1 protein] [gn:atp1:n1129] [gtcf:2.8:12.6] [keggf:14.2] [sgdfc:2.5:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1625	33362500_f2_1	3689	17792	972	324	YNL169C	574	8.9(10)-56	Saccharomyces cerevisiae	[ui:ynl169c] [pn:phosphatidylserine decarboxylase 1:phosphatidylserine decarboxylase proenzyme 1 precursor] [gn:psd1:n1692] [gtcf:2.8:3.4:5.3:8.1:8.2:10.2] [ec:4.1.1.65] [keggf:5.3:8.1] [sgdfc:1.6:1.1:6.4:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3682	12929655_f3_4	3690	17793	1392	464	YNL137C	607	2.7(10)-59	Saccharomyces cerevisiae	[ui:ynl137c] [pn:ribosomal protein, mitochondrial:nam9:n1211:n1840] precursor [gn:nam9:n1211:n1840] [gtcf:2.8:10.4] [keggfc:14.2] [sgdfc:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4489	5272257_f2_6	3691	17794	309	103	YNL066W	293	5.2(10)-26	Saccharomyces cerevisiae	[ui:ynl066w] [pn:involved in the aging process:proteasome component sun4] [gn:sun4:n2411:ynl2411w] [gtcf:2.8:12.13] [keggfc:14.2] [sgdfc:9.7:0:11.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5792	6665902_c3_40	3692	17795	1050	350	YNR041C	884	1.3(10)-88	Saccharomyces cerevisiae	[ui:ynr041c] [pn:para-hydroxybenzoate--polyprenyltransferase:para-hydroxybenzoate--polyprenyltransferase precursor:phb:polyprenyltransferase] [gn:coq2:n3419] [gtcf:2.8:7.1:9.10:9.11:9.12:11.3] [ec:2.5.1.-] [keggfc:7.2:9.13] [sgdfc:1.
CONTIG5748	1250135_c3_23	3693	17796	1494	498	YOL140W	1053	1.6(10)-106	Saccharomyces cerevisiae	[ui:yol140w] [pn:acetylornithine aminotransferase:acetylornithine aminotransferase precursor:acoal] [gn:arg8] [gtcf:2.8:5.16:6.6] [ec:2.6.1.11] [keggfc:5.16] [sgdfc:1.1:9.7:0] [db:gtc-saccharomyces cerevisiae]

CONTIG4945	38887_c3_12	3694	17797	1002	334	YOL096C	727	5.5(10)-72	Saccharomyces cerevisiae	[ui:yol096c] [pn:3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase:hexaprenyldihydroxybenzoate methyltransferase precursor:dihydroxyhexaprenylbenzoate methyltransferase:3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase:dhhb meth
CONTIG5635	34378252_c1_14	3695	17798	1626	542	YOL033W	1090	7.7(10)-118	Saccharomyces cerevisiae	[ui:yol033w] [pn:glutamyl-trna synthetase, mitochondrial:glutamate--trna ligase:glurs] [gn:mse1] [gtcfc:2.8:5.1:9.10:10.6] [ec:6.1.1.17] [keggfc:5.1:9.10:10.1:10.2] [sgdgc:5.4:0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5529	1458318_fl_1	3696	17799	429	143	YOL023W	398	1.6(10)-36	Saccharomyces cerevisiae	[ui:yol023w] [pn:translation initiation factor 2, mitochondrial:initiation factor if-2, mitochondrial precursor:if-2mt] [gn:ifm1] [gtcfc:2.8:10.7] [keggfc:14.2] [sgdgc:5.2:0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5529	21682937_b3_6	3697	17800	1449	483	YOL023W	931	1.3(10)-93	Saccharomyces cerevisiae	[ui:yol023w] [pn:translation initiation factor 2, mitochondrial:initiation factor if-2, mitochondrial precursor:if-2mt] [gn:ifm1] [gtcfc:2.8:10.7] [keggfc:14.2] [sgdgc:5.2:0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5796	25397577_fl_8	3698	17801	1287	429	YOL009C	300	4.7(10)-44	Saccharomyces cerevisiae	[lui.yol009c] [pn:involved in mitochondrial inheritance] [gn:mdm12] [gtcf:2.8] [keggf:14.2] [sgdf:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG623	25506942_fl_1	3699	17802	756	252	YOR017W	177	1.8(10)-12	Saccharomyces cerevisiae	[lui.yor017w] [pn:component of mitochondrial translation system:putative mitochondrial translation system component pet127] [gn:pet127:or26] [gtcf:2.8:10.7] [keggf:14.2] [sgdf:5.3.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
b9x11172.x	21954437_c3_2	3700	17803	783	261	YOR017W	208	8.4(10)-16	Saccharomyces cerevisiae	[lui.yor017w] [pn:component of mitochondrial translation system:putative mitochondrial translation system component pet127] [gn:pet127:or26] [gtcf:2.8:10.7] [keggf:14.2] [sgdf:5.3.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4846	2772530_c1_9	3701	17804	318	106	YOR020C	312	5.2(10)-28	Saccharomyces cerevisiae	[lui.yor020c] [pn:chaperonin, mitochondrial:10 kd heat shock protein, mitochondrial:hsp10:10 kd chaperonin] [gn:hsp10:cpn10:or26] [gtcf:12.7:2.8:10.7:1.1] [keggf:14.2] [sgdf:6.2.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG987	880017_f3_1	3702	17805	429	143	YOR065W	561	2.1(10)-54	Saccharomyces cerevisiae	[lui.yor065w] [pn:cytochrome c1:cytochrome c1, heme protein precursor] [gn:ctc1:cyt1] [gtcf:2.8] [keggf:14.2] [sgdf:5.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2506	20007785_c1_4	3703	17806	549	183	YOR150W	510	5.4(10)-49	Saccharomyces cerevisiae	[ui:yor150w] [pn:similarity to ribosomal protein l13] [gtcf:2.8:10.4] [keggf:14.2] [sgdf:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5467	3023443_c2_17	3704	17807	693	231	YOR158W	218	4.7(10)-18	Saccharomyces cerevisiae	[ui:yor158w] [pn:ribosomal protein, mitochondrial:mitochondrial 40s ribosomal protein precursor] [gn:pet123] [gtcf:2.8:10.4] [keggf:14.2] [sgdf:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5788	29462502_f3_10	3705	17808	1206	402	YOR176W	1254	7.7(10)-128	Saccharomyces cerevisiae	[ui:yor176w] [pn:ferrochelatase precursor:protoheme ferro-lyase:heme synthetase] [gn:hem15] [gtcf:2.8:9.10:9.1:12.6] [ec:4.99.1.1] [keggf:9.10] [sgdf:1.7.1:1.8.1:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4202	26618966_f2_2	3706	17809	663	221	YOR187W	664	2.6(10)-65	Saccharomyces cerevisiae	[ui:yor187w] [pn:translation elongation factor tu, mitochondrial:elongation factor tu, mitochondrial precursor] [gn:tuf1:tufm] [gtcf:2.8:10.7] [keggf:14.2] [sgdf:5.2:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2136	35199025_c2_2	3707	17810	480	160	YOR196C	483	3.8(10)-46	Saccharomyces cerevisiae	[ui:yor196c] [pn:lipoic acid synthase:lipoic acid synthetase precursor:lip-syn] [gn:lip5] [gtcf:2.8:9.10:9.1:1] [keggf:14.2] [sgdf:1.7.1:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2598	32032812_c3_2	3708	17811	1275	425	YOR201C	297	1.1(10)-40	Saccharomyces cerevisiae	[ui:yor201c] [pn:rma:guanosine-2"-o-methyltransferase:ribose large ribosomal rna ribose methylase] [gn:pet56] [gtcf:2.8:3.7:5.11:5.14:9.12:10.3] [ec:2.1.1.-] [keggc:3.7:5.11:5.14:9.13] [sgdfc:4.2.0:
CONTIG1196	1304582_f1_1	3709	17812	1065	355	YOR211C	705	1.2(10)-69	Saccharomyces cerevisiae	[ui:yor211c] [pn:dynammin-like protein:mgm1 protein precursor] [gn:mgm1:yor50-1] [gtcf:2.8] [keggc:14.2] [sgdfc:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3428	31542562_f3_2	3710	17813	1026	342	YOR211C	332	1.2(10)-44	Saccharomyces cerevisiae	[ui:yor211c] [pn:dynammin-like protein:mgm1 protein precursor] [gn:mgm1:yor50-1] [gtcf:2.8] [keggc:14.2] [sgdfc:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4453	30211575_f3_2	3711	17814	372	124	YOR211C	280	2.0(10)-23	Saccharomyces cerevisiae	[ui:yor211c] [pn:dynammin-like protein:mgm1 protein precursor] [gn:mgm1:yor50-1] [gtcf:2.8] [keggc:14.2] [sgdfc:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2021	19743805_f3_1	3712	17815	1161	387	YOR274W	692	2.7(10)-68	Saccharomyces cerevisiae	[ui:yor274w] [pn:isopentenyl-diphosphate:trna isopentenyltransferase:ipp transferase:ipp] [gn:mod5] [gtcf:2.8:10.1:10.2:10.6:14.1] [ec:2.5.1.8] [keggc:14.1] [sgdfc:4.6.0:9.2.0:9.5.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3071	4381436_f3_3	3713	17816	963	321	YOR330C	426	9.0(10)-39	Saccharomyces cerevisiae	[lui:yor330c] [pn:dna-directed dna polymerase gamma catalytic subunit, mitochondrial:dna polymerase gamma:mitochondrial dna polymerase catalytic subunit] [gn:mip1] [gtcf:2.8:4.1:4.2:10.8] [ec:2.7.7.7] [keggf:4.1:4.2] [sgdfc:3.6.0:9.7]
CONTIG5060	21963277_c3_7	3714	17817	2232	744	YOR330C	1455	3.8(10)-149	Saccharomyces cerevisiae	[lui:yor330c] [pn:dna-directed dna polymerase gamma catalytic subunit, mitochondrial:dna polymerase gamma:mitochondrial dna polymerase catalytic subunit] [gn:mip1] [gtcf:2.8:4.1:4.2:10.8] [ec:2.7.7.7] [keggf:4.1:4.2] [sgdfc:3.6.0:9.7]
CONTIG4036	34251377_c1_5	3715	17818	1155	385	YOR334W	780	1.3(10)-77	Saccharomyces cerevisiae	[lui:yor334w] [pn:ma splicing protein and member of the mitochondrial carrier family:mcf:mitochondrial ma splicing protein mrs2 precursor] [gn:mrs2:yor333c] [gtcf:2.8:10.2] [keggf:14.2] [sgdfc:4.9.0:9.7.0] [db:gtc-saccharomyces cer
CONTIG4238	14648436_c3_8	3716	17819	1482	494	YOR355W	329	1.8(10)-29	Saccharomyces cerevisiae	[lui:yor355w] [pn:nam9-1 suppressor:protein] [gn:gds1] [gtcf:2.8] [keggf:14.2] [sgdfc:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2959	31258541_f2_2	3717	17820	183	61	YPL215W	92	0.00067	Saccharomyces cerevisiae	[lui:yp1215w] [pn:required for assembly of cytochrome bc1 complex:protein precursor] [gn:cbp3] [gtcf:2.8:12.16] [keggf:14.2] [sgdfc:6.4.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3142	781256_f2_2	3718	17821	1008	336	YPL215W	736	6.0(10)-73	Saccharomyces cerevisiae	[ui:yp1173w] [pn:required for assembly of cytochrome bc1 complex:protein precursor] [gn:cbp3] [gtcf:2.8:12.16] [keggf:14.2] [sgdf:6.4.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2108	10663437_f1_1	3719	17822	639	213	YPL173W	161	1.2(10)-11	Saccharomyces cerevisiae	[ui:yp1173w] [pn:ribosomal protein yml40, mitochondrial:mitochondrial 60s ribosomal protein [40:ym140] [gn:mrpl40] [gtcf:2.8:10.4] [keggf:14.2] [sgdf:5.1.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5191	15097650_c3_11	3720	17823	336	112	YPL172C	199	2.7(10)-15	Saccharomyces cerevisiae	[ui:yp1172c] [pn:farnesyl transferase:cytochrome c oxidase assembly protein precursor] [gn:cox10] [gtcf:2.8:3.1:9.10:9.11:12.16] [keggf:14.2] [sgdf:1.6.3:1.7.1:6.4.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5559	33773507_f3_13	3721	17824	1167	389	YPL172C	899	3.2(10)-90	Saccharomyces cerevisiae	[ui:yp1172c] [pn:farnesyl transferase:cytochrome c oxidase assembly protein precursor] [gn:cox10] [gtcf:2.8:3.1:9.10:9.11:12.16] [keggf:14.2] [sgdf:1.6.3:1.7.1:6.4.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4714	33400257_f2_2	3722	17825	825	275	YPL132W	764	6.5(10)-76	Saccharomyces cerevisiae	[ui:yp1132w] [pn:cytochrome-c oxidase assembly protein:cytochrome c oxidase assembly protein cox11] [gn:cox11:lp13w] [gtcf:2.8:9.10:9.11:12.16] [keggf:14.2] [sgdf:1.7.1:6.4:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4972	22867143_c1_9	3723	17826	1683	561	YPL104W	678	8.5(10)-67	Saccharomyces cerevisiae	[ui:yp1104w] [pn:aspartate--trna ligase, mitochondrial:aspartyl-trna synthetase, mitochondrial:aspartate--trna ligase:asprs] [gn:msd1:lp5w] [gtcf:2.8:5.2:10.6] [ec:6.1.1.12] [keggf:5.2:10.1:10.2] [sgdf:5.4:0.9:7.0] [db:gtc-saccha]
CONTIG4559	34171950_c2_5	3724	17827	255	85	YPL097W	100	0.00016	Saccharomyces cerevisiae	[ui:yp1097w] [pn:tyrosyl-trna synthetase:tyrosyl-trna synthetase, mitochondrial precursor:tyrosine--trna ligase:tyrrs] [gn:msyl:lp11w] [gtcf:2.8:5.15:10.6] [ec:6.1.1.1] [keggf:5.15:10.1:10.2] [sgdf:5.4:0.9:7.0] [db:gtc-saccharomyc]
CONTIG578	976587_c1_3	3725	17828	537	179	YPL097W	249	1.1(10)-20	Saccharomyces cerevisiae	[ui:yp1097w] [pn:tyrosyl-trna synthetase:tyrosyl-trna synthetase, mitochondrial precursor:tyrosine--trna ligase:tyrrs] [gn:msyl:lp11w] [gtcf:2.8:5.15:10.6] [ec:6.1.1.1] [keggf:5.15:10.1:10.2] [sgdf:5.4:0.9:7.0] [db:gtc-saccharomyc]

CONTIG5813	3912836_c2_44	3726	17829	1164	388	YPL040C	591	8.4(10)-57	Saccharomyces cerevisiae	[ui:yp1040c] [pn:isoleucine--trna ligase, mitochondrial:isoleucyl-trna synthetase, mitochondrial:isoleucine--trna ligase:ilers] [gn:ism1:p7102] [gtcf:2.8:5.7:10.6] [ec:6.1.1.5] [keggfc:5.7:10.1:10.2] [sgdfc:5.4:0.9:7.0] [db:gtc-sacch
CONTIG5813	258387_c1_33	3727	17830	1821	607	YPL040C	1204	1.5(10)-122	Saccharomyces cerevisiae	[ui:yp1040c] [pn:isoleucine--trna ligase, mitochondrial:isoleucyl-trna synthetase, mitochondrial:isoleucine--trna ligase:ilers] [gn:ism1:p7102] [gtcf:2.8:5.7:10.6] [ec:6.1.1.5] [keggfc:5.7:10.1:10.2] [sgdfc:5.4:0.9:7.0] [db:gtc-sacch
CONTIG5153	1181552_f2_3	3728	17831	2166	722	YPL029W	1113	6.7(10)-113	Saccharomyces cerevisiae	[ui:yp1029w] [pn:atp-dependent rna helicase, mitochondrial:mitochondrial atp-dependent rna helicase suv3 precursor] [gn:suv3:lpb2w] [gtcf:2.8:4.4:10.10:10.2:10.3:10.7] [keggfc:14.2] [sgdfc:1.3:6.4:2.0:4.9:0.5:3.0:9.7:0] [db:gtc-sacch
CONTIG3664	1550_c2_8	3729	17832	630	210	YPL013C	279	1.6(10)-24	Saccharomyces cerevisiae	[ui:yp1013c] [pn:ribosomal protein s16, mitochondrial] [gtcf:2.8:10.4] [keggfc:14.2] [sgdfc:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5198	31913311_c1_8	3730	17833	1302	434	YPR024W	1043	1.8(10)-105	Saccharomyces cerevisiae	[ui:ypr024w] [pn:protease of the sec18/cdc48/pas1 family of atpases:aaa:yme1 protein:tat-binding homolog 11:osd1 protein] [gn:yme1:ytal1:osd1:yp9367] [gtcf:2.8:10.11:12.16] [ec:3.4.24.-] [keggf:14.1] [sgdfc:6.4.0.6.5.3.9.7.0] [db:gt
CONTIG816	33492754_c2_5	3731	17834	909	303	YPR024W	978	1.3(10)-98	Saccharomyces cerevisiae	[ui:ypr024w] [pn:protease of the sec18/cdc48/pas1 family of atpases:aaa:yme1 protein:tat-binding homolog 11:osd1 protein] [gn:yme1:ytal1:osd1:yp9367] [gtcf:2.8:10.11:12.16] [ec:3.4.24.-] [keggf:14.1] [sgdfc:6.4.0.6.5.3.9.7.0] [db:gt
CONTIG5155	5353307_f1_1	3732	17835	606	202	YPR037C	351	3.7(10)-32	Saccharomyces cerevisiae	[ui:ypr037c] [pn:similarity to erv1p and rat alr protein] [gtcf:2.8] [keggf:14.2] [sgdfc:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4428	14100281_f3_4	3733	17836	357	119	YPR047W	167	8.9(10)-12	Saccharomyces cerevisiae	[ui:ypr047w] [pn:phenylalanine--trna ligase alpha chain, mitochondrial] [gn:msf1] [gtcf:2.8:5.15:10.6:10.7:11.1] [ec:6.1.1.20] [keggf:5.15:10.1:10.2] [sgdfc:5.4.0.6.2.0:9.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5336	26265627_c2_12	3734	17837	918	306	YPR047W	871	3.0(10)-87	Saccharomyces cerevisiae	[ui:ypr047w] [pn:phenylalanine--tRNA ligase alpha chain, mitochondrial] [gn:mst1] [gtcf:2.8:5.15:10.6:10.7:11.1] [ec:6.1.1.20] [keggf:5.15:10.1:10.2] [sgdf:5.4:0.6:2.0:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2365	16431388_c3_5	3735	17838	528	176	YPR155C	119	2.0(10)-15	Saccharomyces cerevisiae	[ui:ypr155c] [pn:control of mitochondrial synthesis of atp6p and atp8p] [gn:nca2] [gtcf:2.8] [keggf:14.2] [sgdf:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5107	156261_c3_10	3736	17839	1605	535	YPR155C	193	5.7(10)-12	Saccharomyces cerevisiae	[ui:ypr155c] [pn:control of mitochondrial synthesis of atp6p and atp8p] [gn:nca2] [gtcf:2.8] [keggf:14.2] [sgdf:9.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5523	21914062_f1_3	3737	17840	387	129	YPR166C	292	6.7(10)-26	Saccharomyces cerevisiae	[ui:ypr166c] [pn:ribosomal protein s14:mitochondrial 40s ribosomal protein mrp2] [gn:mrp2:p9325] [gtcf:2.8:10.4] [keggf:14.2] [sgdf:5.1:0.9:7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4269	12288260_c1_3	3738	17841	1242	414	YDL107W	266	2.8(10)-38	Saccharomyces cerevisiae	[ui:ydl107w] [pn:ser/thr protein kinase:mss2 protein] [gn:mss2:d2340] [gtcf:2.8:12.13] [keggf:14.2] [sgdf:2.5:0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3724	1586_f3_2	3739	17842	1452	484	YEL053C	247	1.8(10)-18	Saccharomyces cerevisiae	[ui:yel053c] [pn:glucose-repressible protein:glucose repressible protein] [gn:mak10] [gtcf:2.8] [keggf:14.2] [sgdf:2.5:0] [db:gtc-saccharomyces cerevisiae]

CONTIG4466	26345312_f3_4	3740	17843	579	193	YEL053C	94	0.05199	Saccharomyces cerevisiae	[ui:yel053c] [pn:glucose-repressible protein:glucose repressible protein] [gn:mak10] [gtcf:2.8] [keggf:14.2] [sgdfc:2.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4070	20759813_c3_8	3741	17844	528	176	YGR062C	133	1.8(10)-8	Saccharomyces cerevisiae	[ui:ygr062c] [pn:required for activity of mitochondrial cytochrome oxidase:cytochrome c oxidase assembly protein cox18 precursor] [gn:cox18:g4532] [gtcf:2.8] [keggf:14.2] [sgdfc:2.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5713	26199067_f3_8	3742	17845	525	175	YGR062C	187	1.7(10)-14	Saccharomyces cerevisiae	[ui:ygr062c] [pn:required for activity of mitochondrial cytochrome oxidase:cytochrome c oxidase assembly protein cox18 precursor] [gn:cox18:g4532] [gtcf:2.8] [keggf:14.2] [sgdfc:2.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4949	959687_f1_2	3743	17846	246	82	YLL009C	102	9.3(10)-6	Saccharomyces cerevisiae	[ui:yll009c] [pn:interacts genetically with sco1 and sco2 in cytochrome oxidase assembly] [gn:cox17] [gtcf:2.8:12.16:12.6] [keggf:14.2] [sgdfc:1.8.1:2.5.0:6.4.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
blx17891.y	6033442_f1_1	3744	17847	519	173	YML125C	454	4.5(10)-43	Saccharomyces cerevisiae	[ui:yml125c] [pn:strong similarity to cytochrome-b5- and nitrate reductases] [gtcf:2.8] [keggf:14.2] [sgdfc:2.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1595	2054517_c1_4	3745	17848	660	220	YMR073C	186	4.0(10)-19	Saccharomyces cerevisiae	[ui:ymr073c] [pn:weak similarity to c-terminal part of cytochrome b5 and b2] [gtcf:2.8] [keggf:14.2] [sgdfc:2.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2926	36444568_c2_5	3746	17849	852	284	YMR145C	759	2.2(10)-75	Saccharomyces cerevisiae	[ui:ymr145c] [pn:strong similarity to nadh dehydrogenase:ubiquinone:hypothetical 62.8 kd protein in mds1-swp1 intergenic region] [gn:ym9375] [gtcf:2.8:9.12] [keggf:14.2] [sgdfc:2.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5718	12271933_c2_20	3747	17850	582	194	YMR165C	333	2.2(10)-33	Saccharomyces cerevisiae	[ui:ymr165c] [pn:involved in plasmid maintenance, respiration and cell proliferation:smp2 protein] [gn:smp2:ym8520] [gtcf:2.8:12.8] [keggf:14.2] [sgdfc:2.5.0:3.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5321	4375675_c3_32	3748	17851	1203	401	YNL118C	662	9.0(10)-65	Saccharomyces cerevisiae	[ui:ynl118c] [pn:suppressor protein of a yeast pet mutant:psu1 protein] [gn:psu1:n1917] [gtcf:2.8] [keggf:14.2] [sgdfc:2.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5628	24266511_fl_4	3749	17852	1905	635	YOR356W	1905	8.0(10)-197	Saccharomyces cerevisiae	[ui:yor356w] [pn:strong similarity to human electron transfer flavoprotein-ubiquinone oxidoreductase:strong similarity to human electron transfer flavoprotein- ubiquinone oxidoreductase] [gtcf:2.8:9.12] [keggf:14.2] [sgdfc:2.5.0] [d

b3x16938.y	14536001_c3_5	3750	17853	336	112	YPR004C	147	6.7(10)-10	Saccharomyces cerevisiae	[ui:ypr004c] [pn:strong similarity to electron transfer flavoproteins alpha chain] [gtcf:2.8] [keggf:14.2] [sgdfc:2.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4428	13864407_f3_3	3751	17854	861	287	YPR048W	347	4.5(10)-31	Saccharomyces cerevisiae	[ui:ypr048w] [pn:similarity to m.domestica nadph-- ferrihemoprotein reductase and mammalian nitric-oxide synthases] [gtcf:2.8] [keggf:14.2] [sgdfc:2.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4428	22034632_fl_2	3752	17855	1068	356	YPR048W	628	1.7(10)-61	Saccharomyces cerevisiae	[ui:ypr048w] [pn:similarity to m.domestica nadph-- ferrihemoprotein reductase and mammalian nitric-oxide synthases] [gtcf:2.8] [keggf:14.2] [sgdfc:2.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4071	22540967_f3_5	3753	17856	2067	689	YKL182W	2276	3.8(10)-236	Saccharomyces cerevisiae	[ui:ykl182w] [pn:fatty-acyl-coa synthase, beta chain:fatty acid synthase, subunit beta:contains 3-hydroxypalmitoyl-acyl-carrier-protein dehydratase enoyl-acyl-carrier-protein reductase (nadh) acyl-carrier-protein acetyltransferase acyl
CONTIG3036	3944006_f3_3	3754	17857	1185	395	YKL182W	1029	1.1(10)-102	Saccharomyces cerevisiae	[ui:ykl182w] [pn:fatty-acyl-coa synthase, beta chain:fatty acid synthase, subunit beta:contains 3-hydroxypalmitoyl-acyl-carrier-protein dehydratase enoyl-acyl-carrier-protein reductase (nadh) acyl-carrier-protein acetyltransferase acyl

CONTIG2315	23938329_c1_3	3755	17858	909	303	YKL182W	968	3.5(10)-96	Saccharomyces cerevisiae	[ui:ykl182w] [pn:fatty-acyl-coa synthase, beta chain:fatty acid synthase, subunit beta:contains 3-hydroxypalmitoyl-acyl-carrier-protein dehydratase enoyl-acyl-carrier-protein reductase (nadh) acyl-carrier-protein acetyltransferase acyl
CONTIG2544	1959375_c2_5	3756	17859	1209	403	YPL231W	1211	2.1(10)-122	Saccharomyces cerevisiae	[ui:ypl231w] [pn:fatty-acyl-coa synthase, alpha chain:fatty acid synthase, subunit alpha:contains:ec 1.1.1.100, and ec 2.3.1.41] [gn:fas2] [gtcfc:3.1:3.4:8.1:8.2:12.16] [ec:2.3.1.86] [keggfc:3.1] [sgdfe:1.6.1:6.4.0:9.2.0] [db:gtc-sacc
CONTIG3183	269442_f1_1	3757	17860	1242	414	YPL231W	1286	1.3(10)-130	Saccharomyces cerevisiae	[ui:ypl231w] [pn:fatty-acyl-coa synthase, alpha chain:fatty acid synthase, subunit alpha:contains:ec 1.1.1.100, and ec 2.3.1.41] [gn:fas2] [gtcfc:3.1:3.4:8.1:8.2:12.16] [ec:2.3.1.86] [keggfc:3.1] [sgdfe:1.6.1:6.4.0:9.2.0] [db:gtc-sacc
CONTIG3183	30096938_f3_5	3758	17861	222	74	YPL231W	132	3.1(10)-7	Saccharomyces cerevisiae	[ui:ypl231w] [pn:fatty-acyl-coa synthase, alpha chain:fatty acid synthase, subunit alpha:contains:ec 1.1.1.100, and ec 2.3.1.41] [gn:fas2] [gtcfc:3.1:3.4:8.1:8.2:12.16] [ec:2.3.1.86] [keggfc:3.1] [sgdfe:1.6.1:6.4.0:9.2.0] [db:gtc-sacc

CONTIG3995	36366563_cl_8	3759	17862	1131	377	YPL231W	1256	2.6(10)-127	Saccharomyces cerevisiae	[ui:yp1231w] [pn:fatty-acyl-coa synthase, alpha chain:fatty acid synthase, subunit alpha:contains:ec 1.1.1.100, and ec 2.3.1.41] [gn:fas2] [gtcf:3.1:3.4.8.1:8.2:12.16] [ec:2.3.1.86] [keggfc:3.1] [sgdfc:1.6.1:6.4.0:9.2.0] [db:gtc-sacc]
CONTIG679	26376953_f2_3	3760	17863	240	80	YPL231W	320	3.2(10)-27	Saccharomyces cerevisiae	[ui:yp1231w] [pn:fatty-acyl-coa synthase, alpha chain:fatty acid synthase, subunit alpha:contains:ec 1.1.1.100, and ec 2.3.1.41] [gn:fas2] [gtcf:3.1:3.4.8.1:8.2:12.16] [ec:2.3.1.86] [keggfc:3.1] [sgdfc:1.6.1:6.4.0:9.2.0] [db:gtc-sacc]
CONTIG679	24610787_f3_4	3761	17864	1095	365	YPL231W	1397	5.5(10)-143	Saccharomyces cerevisiae	[ui:yp1231w] [pn:fatty-acyl-coa synthase, alpha chain:fatty acid synthase, subunit alpha:contains:ec 1.1.1.100, and ec 2.3.1.41] [gn:fas2] [gtcf:3.1:3.4.8.1:8.2:12.16] [ec:2.3.1.86] [keggfc:3.1] [sgdfc:1.6.1:6.4.0:9.2.0] [db:gtc-sacc]

CONTIG2925	20347787_c3_6	3762	17865	1185	395	YDL090C	231	4.2(10)-18	Saccharomyces cerevisiae	[ui:ydl090c] [pn:protein farnesyltransferase, beta subunit:protein farnesyltransferase beta subunit:caax farnesyltransferase beta subunit:ras proteins prenyltransferase:flase-beta] [gn:ram1:dpr1:ste16:scg2:d2412] [gtcf:3.1:7.1:9.12:10]
b3x16082.x	1994166_f2_1	3763	17866	288	96	YDL090C	135	2.2(10)-8	Saccharomyces cerevisiae	[ui:ydl090c] [pn:protein farnesyltransferase, beta subunit:protein farnesyltransferase beta subunit:caax farnesyltransferase beta subunit:ras proteins prenyltransferase:flase-beta] [gn:ram1:dpr1:ste16:scg2:d2412] [gtcf:3.1:7.1:9.12:10]
CONTIG3892	14344057_f1_1	3764	17867	1425	475	YDL040C	1042	2.2(10)-105	Saccharomyces cerevisiae	[ui:ydl040c] [pn:protein n-acetyltransferase subunit:n-terminal, alpha-amino, acetyltransferase 1] [gn:nat1:aaa1:d2720] [gtcf:3.1:10.7:14.1] [ec:2.3.1.88] [keggfc:14.1] [sgdfc:1.6.3:5.0:6.3:0:9.2.

CONTIG4324	24881577_c2_9	3765	17868	807	269	YDL040C	237	7.2(10)-19	Saccharomyces cerevisiae	[ui:ydl040c] [pn:protein n-acetyltransferase subunit:n-terminal, alpha-amino, acetyltransferase 1] [gn:nat1:aaal:d2720] [gtcf:3.1:10.7:14.1] [ec:2.3.1.88] [keggfc:14.1] [sgdfc:1.6.3:5.0:6.3:0:9.2.]
CONTIG5041	10663925_f3_4	3766	17869	1080	360	YDR331W	1086	4.9(10)-110	Saccharomyces cerevisiae	[ui:ydr331w] [pn:essential for gpi anchor attachment:hypothetical 47.4 kd protein in pas3 3"region] [gn:gpi8.d9798] [gtcf:3.1:10.7:12.16] [keggfc:14.2] [sgdfc:1.6.3:6.3:0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1277	24042550_c3_3	3767	17870	408	136	YDR410C	196	1.2(10)-19	Saccharomyces cerevisiae	[ui:ydr410c] [pn:farnesyl cysteine carboxyl-methyltransferase:protein-s isoprenylcysteine o-methyltransferase:isoprenylcysteine carboxylmethyltransferase] [gn:ste14.d9461] [gtcf:3.1:10.7] [ec:2.1.1.100] [keggfc:14.1] [sgdfc:1.6.3:6.3]
CONTIG3528	25549090_c2_5	3768	17871	843	281	YDR410C	191	3.3(10)-15	Saccharomyces cerevisiae	[ui:ydr410c] [pn:farnesyl cysteine carboxyl-methyltransferase:protein-s isoprenylcysteine o-methyltransferase:isoprenylcysteine carboxylmethyltransferase] [gn:ste14.d9461] [gtcf:3.1:10.7] [ec:2.1.1.100] [keggfc:14.1] [sgdfc:1.6.3:6.3]

CONTIG2198	21517168_f2_1	3769	17872	912	304	YER015W	723	1.3(10)-71	Saccharomyces cerevisiae	[ui:yer015w] [pn:long-chain-fatty-acid--coa ligase:long-chain-fatty-acid--coa ligase 2:long-chain acyl-coa synthetase 2:fatty acid activator 2] [gn:faa2:fam1] [gtcf:3.1.3.2:12.2:12.6] [ec:6.2.1.3] [keggfc:3.2] [sgdfc:1.6.3:1.6.5:8.4]
CONTIG3922	4773937_f1_1	3770	17873	975	325	YER015W	389	2.2(10)-35	Saccharomyces cerevisiae	[ui:yer015w] [pn:long-chain-fatty-acid--coa ligase:long-chain-fatty-acid--coa ligase 2:long-chain acyl-coa synthetase 2:fatty acid activator 2] [gn:faa2:fam1] [gtcf:3.1.3.2:12.2:12.6] [ec:6.2.1.3] [keggfc:3.2] [sgdfc:1.6.3:1.6.5:8.4]
CONTIG4532	12625281_f1_1	3771	17874	1380	460	YER015W	971	7.5(10)-98	Saccharomyces cerevisiae	[ui:yer015w] [pn:long-chain-fatty-acid--coa ligase:long-chain-fatty-acid--coa ligase 2:long-chain acyl-coa synthetase 2:fatty acid activator 2] [gn:faa2:fam1] [gtcf:3.1.3.2:12.2:12.6] [ec:6.2.1.3] [keggfc:3.2] [sgdfc:1.6.3:1.6.5:8.4]
CONTIG4868	820425_f3_4	3772	17875	186	62	YER015W	128	2.7(10)-7	Saccharomyces cerevisiae	[ui:yer015w] [pn:long-chain-fatty-acid--coa ligase:long-chain-fatty-acid--coa ligase 2:long-chain acyl-coa synthetase 2:fatty acid activator 2] [gn:faa2:fam1] [gtcf:3.1.3.2:12.2:12.6] [ec:6.2.1.3] [keggfc:3.2] [sgdfc:1.6.3:1.6.5:8.4]

CONTIG5092	10976502_c1_10	3773	17876	1851	617	YER015W	718	4.9(10)-71	Saccharomyces cerevisiae	[ui:yer015w] [pn:long-chain-fatty-acid--coa ligase:long-chain-fatty-acid--coa ligase 2:long-chain acyl-coa synthetase 2:fatty acid activator 2] [gn:faa2:fam1] [gtcf:3.1:3.2:12.2:12.6] [ec:6.2.1.3] [keggfc:3.2] [sgdfc:1.6.3:1.6.5:8.4]
CONTIG5818	23447052_f1_3	3774	17877	765	255	YER015W	167	2.1(10)-16	Saccharomyces cerevisiae	[ui:yer015w] [pn:long-chain-fatty-acid--coa ligase:long-chain-fatty-acid--coa ligase 2:long-chain acyl-coa synthetase 2:fatty acid activator 2] [gn:faa2:fam1] [gtcf:3.1:3.2:12.2:12.6] [ec:6.2.1.3] [keggfc:3.2] [sgdfc:1.6.3:1.6.5:8.4]
CONTIG5818	30173825_f2_15	3775	17878	1494	498	YER015W	919	2.5(10)-92	Saccharomyces cerevisiae	[ui:yer015w] [pn:long-chain-fatty-acid--coa ligase:long-chain-fatty-acid--coa ligase 2:long-chain acyl-coa synthetase 2:fatty acid activator 2] [gn:faa2:fam1] [gtcf:3.1:3.2:12.2:12.6] [ec:6.2.1.3] [keggfc:3.2] [sgdfc:1.6.3:1.6.5:8.4]
b2x15869.x	13788931_f2_1	3776	17879	483	161	YGL155W	137	1.0(10)-8	Saccharomyces cerevisiae	[ui:ygl155w] [pn:geranylgeranyltransferase beta subunit:type i proteins geranylgeranyltransferase beta subunit:type i protein geranylgeranyltransferase beta subunit:gggtase-i-beta:pggt:ras proteins geranylgeranyltransferase beta subunit]

b1x18944.y	866677_c2_1	3777	17880	477	159	YGL155W	206	2.5(10)-16	Saccharomyces cerevisiae	[ui:ygl155w] [pn:geranylgeranyltransferase beta subunit:type i proteins geranylgeranyltransferase beta subunit:type i protein geranyl-geranyltransferase beta subunit:gggtase-i-beta:pggt:ras proteins geranylgeranyltransferase beta subunit]
CONTIG5696	14492952_f2_5	3778	17881	525	175	YHR013C	538	5.7(10)-52	Saccharomyces cerevisiae	[ui:yhr013c] [pn:protein n-acetyltransferase subunit:n-terminal acetyltransferase complex subunit:arrest- defective protein 1] [gn:ard1] [gicfc:3.1:10.7:12.8] [keggfc:14.2] [sgdgc:1.6.3.3.8.0.6.3.0.9.2.0] [db:gic-saccharomyces cerevis]
b3x16013.y	21963942_f1_1	3779	17882	294	98	YHR013C	182	3.1(10)-14	Saccharomyces cerevisiae	[ui:yhr013c] [pn:protein n-acetyltransferase subunit:n-terminal acetyltransferase complex subunit:arrest- defective protein 1] [gn:ard1] [gicfc:3.1:10.7:12.8] [keggfc:14.2] [sgdgc:1.6.3.3.8.0.6.3.0.9.2.0] [db:gic-saccharomyces cerevis]
CONTIG2298	12791267_f2_1	3780	17883	543	181	YJL031C	116	3.3(10)-9	Saccharomyces cerevisiae	[ui:yjl031c] [pn:geranylgeranyltransferase, alpha chain:type ii proteins geranylgeranyltransferase alpha subunit:type ii protein geranyl-geranyltransferase alpha subunit:gggtase-ii-alpha:pggt:ypt1/sec4 proteins geranylgeranyltransferas

CONTIG1168	21485635_c3_3	3781	17884	792	264	YJR066W	202	1.1(10)-18	Saccharomyces cerevisiae	[ui:yjr066w] [pn:phosphatidylinositol 3-kinase:phosphatidylinositol 3-kinase:tor1:pi3-kinase:ptdins-3-kinase:pi3k] [gn:tor1:dr1:j1803] [gtcf:3.1:8.1:10.7:12.8] [ec:2.7.1.137] [keggf:8.1] [sgdfe:1.6.3.3.8.0.5.5.0] [db:gtc-saccharomy
b2x15416.x	31273942_f2_1	3782	17885	816	272	YJR066W	832	1.6(10)-81	Saccharomyces cerevisiae	[ui:yjr066w] [pn:phosphatidylinositol 3-kinase:phosphatidylinositol 3-kinase:tor1:pi3-kinase:ptdins-3-kinase:pi3k] [gn:tor1:dr1:j1803] [gtcf:3.1:8.1:10.7:12.8] [ec:2.7.1.137] [keggf:8.1] [sgdfe:1.6.3.3.8.0.5.5.0] [db:gtc-saccharomy
CONTIG1565	16220261_c3_2	3783	17886	444	148	YKL019W	214	1.3(10)-17	Saccharomyces cerevisiae	[ui:ykl019w] [pn:protein farnesyltransferase, alpha subunit:protein farnesyltransferase alpha subunit:caax farnesyltransferase alpha subunit:ras proteins prenyltransferase:ftase-alpha] [gn:ram2] [gtcf:3.1:7.1:9.12:10.7:11.3] [ec:2.5.

CONTIG1565	4688312_c3_1	3784	17887	231	77	YKL019W	153	1.2(10)-10	Saccharomyces cerevisiae	[ui:ykl019w] [pn:protein farnesyltransferase, alpha subunit:protein farnesyltransferase alpha subunit:caax farnesyltransferase alpha subunit:ras proteins prenyltransferase:fase-alpha] [gn:ram2] [gtcf:3.1:7.1:9.12:10.7:11.3] [ec:2.5.]
CONTIG1936	24665901_c1_4	3785	17888	471	157	YLR088W	324	1.3(10)-28	Saccharomyces cerevisiae	[ui:ylr088w] [pn:required for attachment of gpi anchor onto proteins:gaal protein] [gn:gaa1:end2:19449] [gtcf:3.1:10.7:12.16:12.6] [keggc:14.2] [sgdf:1.6.3:6.3:0.8:7.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG410	24797067_c3_1	3786	17889	726	242	YLR195C	637	1.8(10)-62	Saccharomyces cerevisiae	[ui:ylr195c] [pn:n-myristoyltransferase:glycylpeptide n-tetradecanoyltransferase:peptide n-myristoyltransferase:myristoyl-coa:protein n-myristoyltransferase:nmt] [gn:nmt1:cdc72:18167] [gtcf:3.1:10.7:14.1] [ec:2.3.1.97] [keggc:14.1]
b9x13972.y	4070152_c1_2	3787	17890	630	210	YMR013C	129	1.3(10)-7	Saccharomyces cerevisiae	[ui:ymr013c] [pn:dolichol kinase] [gn:sec59:ym8270] [gtcf:3.1:7.1:11.3:12.15:12.16] [ec:2.7.1.108] [keggc:7.2] [sgdf:1.6.3:3.4:0.9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2707	4688932_c3_6	3788	17891	972	324	YMR246W	886	7.7(10)-89	Saccharomyces cerevisiae	[ui:ymr246w] [pn:long-chain-fatty-acid--coa ligase:long-chain-fatty-coa synthetase 4:long-chain acyl-coa synthetase 4:fatty acid activator 4] [gn:faa4:ym9408] [gtcf:3.1:3.2:3.4:8.1:8.2:12.2] [ec:6.2.1.3] [keggfc:3.2] [sgdfc:1.6.1:1]
CONTIG4397	984700_f3_2	3789	17892	1038	346	YOR317W	1076	5.7(10)-109	Saccharomyces cerevisiae	[ui:yor317w] [pn:long-chain-fatty-acid--coa ligase:long-chain-fatty-coa synthetase 1:fatty acid activator 1] [gn:faa1:o6136] [gtcf:3.1:3.2:12.2] [ec:6.2.1.3] [keggfc:3.2] [sgdfc:1.6.3:1.6.5] [db:gt]
CONTIG5608	12689637_c1_12	3790	17893	2031	677	YOR370C	1133	5.2(10)-115	Saccharomyces cerevisiae	[ui:yor370c] [pn:geranylgeranyltransferase regulatory subunit:rab proteins geranylgeranyltransferase component a:rab escort protein:rep] [gn:msi4:mrs6] [gtcf:3.1:10.7] [keggfc:14.2] [sgdfc:1.6.3:6.3.0] [db:gtc-saccharomyces cerevisia]
CONTIG4727	25571936_f2_1	3791	17894	630	210	YPR176C	650	7.9(10)-64	Saccharomyces cerevisiae	[ui:ypr176c] [pn:geranylgeranyltransferase type ii beta subunit:type ii proteins geranylgeranyltransferase beta subunit:type ii protein geranylgeranyltransferase beta subunit:ggatase-ii-beta:pggt:ypt1/sec4 proteins geranylgeranyltransf

CONTIG5261	30478927_fl_3	3792	17895	426	142	YPR176C	155	7.7(10)-11	Saccharomyces cerevisiae	[ui:ypr176c] [pn:geranylgeranyltransferase type ii beta subunit: type ii proteins geranylgeranyltransferase beta subunit: type ii protein geranylgeranyltransferase beta subunit: ggtase-ii-beta: pggt: ypt1/sec4 proteins geranylgeranyltransf
CONTIG1764	25976412_fl_1	3793	17896	672	224	YDR058C	441	1.1(10)-41	Saccharomyces cerevisiae	[ui:ydr058c] [pn:lipase 2: triacylglycerol lipase] [gn:tg2.yd9609] [gtcf:3.2:8.1] [ec:3.1.1.3] [keggfc:8.1] [sgdfc:1.6.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2680	20394002_fl_1	3794	17897	861	287	YJL068C	629	1.3(10)-61	Saccharomyces cerevisiae	[ui:yjl068c] [pn:strong similarity to human esterase d: hypothetical 33.9 kd esterase in scp160-mrpl8 intergenic region] [gn:j1102:hre299] [gtcf:3.2] [ec:3.1.1.1] [keggfc:14.1] [sgdfc:1.6.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1156	9979142_fl_1	3795	17898	621	207	YKR031C	203	7.7(10)-15	Saccharomyces cerevisiae	[ui:ykr031c] [pn:phospholipase d: meiosis-specific sporulation protein] [gn:spo14] [gtcf:3.2:12.15] [keggfc:14.2] [sgdfc:1.6.2:3.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2461	23652262_c1_3	3796	17899	1089	363	YKR031C	973	5.0(10)-97	Saccharomyces cerevisiae	[ui:ykr031c] [pn:phospholipase d: meiosis-specific sporulation protein] [gn:spo14] [gtcf:3.2:12.15] [keggfc:14.2] [sgdfc:1.6.2:3.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4483	9806677_c1_14	3797	17900	603	201	YKR031C	488	3.5(10)-45	Saccharomyces cerevisiae	[ui:ykr031c] [pn:phospholipase d:meiosis-specific sporulation protein] [gn:spo14] [gtcfc:3.2:12.15] [keggfc:14.2] [sgdgc:1.6.2:3.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4483	11959836_c3_18	3798	17901	858	286	YKR031C	218	6.0(10)-21	Saccharomyces cerevisiae	[ui:ykr031c] [pn:phospholipase d:meiosis-specific sporulation protein] [gn:spo14] [gtcfc:3.2:12.15] [keggfc:14.2] [sgdgc:1.6.2:3.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5808	9789126_fl_3	3799	17902	1593	531	YLR020C	368	7.0(10)-34	Saccharomyces cerevisiae	[ui:ykr020c] [pn:similarity to triacylglycerol lipase] [gtcfc:3.2] [keggfc:14.2] [sgdgc:1.6.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3882	892182_c2_5	3800	17903	1239	413	YMR006C	707	7.2(10)-70	Saccharomyces cerevisiae	[ui:ykr006c] [pn:strong similarity to plb1p] [gtcfc:3.2] [keggfc:14.2] [sgdgc:1.6.2] [db:gtc-saccharomyces cerevisiae]
CONTIG620	26760175_c2_5	3801	17904	186	62	YMR006C	117	3.8(10)-6	Saccharomyces cerevisiae	[ui:ykr006c] [pn:strong similarity to plb1p] [gtcfc:3.2] [keggfc:14.2] [sgdgc:1.6.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5474	6665938_c1_10	3802	17905	1833	611	YMR008C	1218	5.0(10)-124	Saccharomyces cerevisiae	[ui:ykr008c] [pn:lysophospholipase:lysophospholipase precursor:phospholipase b] [gn:plb1:ym8270] [gtcfc:3.2:8.4:11.1] [ec:3.1.1.5] [keggfc:8.4] [sgdgc:1.6.2:9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5527	22360301_f1_1	3803	17906	1914	638	YMR008C	1603	8.0(10)-165	Saccharomyces cerevisiae	[ui:ymr008c] [pn:lysophospholipase:lysophospholipase precursor:phospholipase b] [gn:plb1:ym8270] [gtcf:3.2:8.4:1.1] [ec:3.1.1.5] [keggfc:8.4] [sgdfc:1.6.2:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG620	33417768_c2_6	3804	17907	627	209	YMR008C	285	3.1(10)-24	Saccharomyces cerevisiae	[ui:ymr008c] [pn:lysophospholipase:lysophospholipase precursor:phospholipase b] [gn:plb1:ym8270] [gtcf:3.2:8.4:1.1] [ec:3.1.1.5] [keggfc:8.4] [sgdfc:1.6.2:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4295	20507697_c2_6	3805	17908	990	330	YNL012W	484	3.1(10)-46	Saccharomyces cerevisiae	[ui:ynl012w] [pn:transcriptional regulator involved in sporulation:sporulation protein spo1] [gn:spo1:n2858] [gtcf:3.2:10.1:10.2:12.15:12.8] [keggfc:14.2] [sgdfc:1.6.2:3.4.0:3.8.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3890	25627002_f2_1	3806	17909	1587	529	YOL011W	1135	3.2(10)-115	Saccharomyces cerevisiae	[ui:yol011w] [pn:strong similarity to phospholipases] [gtcf:3.2] [keggfc:14.2] [sgdfc:1.6.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3994	24641561_c1_6	3807	17910	609	203	YOL011W	217	7.0(10)-17	Saccharomyces cerevisiae	[ui:yol011w] [pn:strong similarity to phospholipases] [gtcf:3.2] [keggfc:14.2] [sgdfc:1.6.2] [db:gtc-saccharomyces cerevisiae]

CONTIG5072	3751_c2_4	3808	17911	2142	714	YOL011W	928	2.7(10)-93	Saccharomyces cerevisiae	[ui:yol011w] [pn:strong similarity to phospholipases] [gtcf:3.2] [keggfc:14.2] [sgdfc:1.6.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2195	20319377_f3_3	3809	17912	306	102	YGR175C	321	1.0(10)-28	Saccharomyces cerevisiae	[ui:ygr175c] [pn:squalene monooxygenase:squalene epoxidase:se] [gn:erg1] [gtcf:3.4.8.1:8.2:9.13:12.16] [ec:1.14.99.7] [keggfc:3.4.9.11] [sgdfc:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2588	5875938_f2_1	3810	17913	255	85	YHR072W	286	3.0(10)-24	Saccharomyces cerevisiae	[ui:yhr072w] [pn:lanosterol synthase:oxidosqualene--lanosterol cyclase:2,3-epoxysqualene--lanosterol cyclase:osc] [gn:erg7] [gtcf:3.4.8.1:8.2:12.16] [ec:5.4.99.7] [keggfc:3.4] [sgdfc:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG515	21932809_c1_1	3811	17914	747	249	YHR072W	765	5.0(10)-76	Saccharomyces cerevisiae	[ui:yhr072w] [pn:lanosterol synthase:oxidosqualene--lanosterol cyclase:2,3-epoxysqualene--lanosterol cyclase:osc] [gn:erg7] [gtcf:3.4.8.1:8.2:12.16] [ec:5.4.99.7] [keggfc:3.4] [sgdfc:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3232	4772512_f3_5	3812	17915	1218	406	YHR190W	1129	1.3(10)-114	Saccharomyces cerevisiae	[ui:yhr190w] [pn:farnesyl-diphosphate farnesyltransferase:squalene synthetase:sqs:ss:fpp:fpp farnesyltransferase] [gn:erg9] [gtcf:3.4.8.1:8.2.9.13:12.16] [ec:2.5.1.21] [keggf:3.4.9.11] [sgdf:1.6.1:9.4.0] [db:gtc-saccharomyces cerev
CONTIG5151	23570892_c3_7	3813	17916	1224	408	YJL167W	1366	1.1(10)-139	Saccharomyces cerevisiae	[ui:yjl167w] [pn:farnesyl-pyrophosphate synthetase:farnesyl pyrophosphate synthetase:fpp synthetase:fps:farnesyl diphosphate synthetase:dimethylallyltransferase/geranyltransferase] [gn:fpp1:fds1:bot3:erg20:j0525] [gtcf:3.4.8.1:
CONTIG2477	35369020_f2_1	3814	17917	942	314	YLR450W	961	8.6(10)-97	Saccharomyces cerevisiae	[ui:ylr450w] [pn:3-hydroxy-3-methylglutaryl-coenzyme a reductase 2:hmg-coa reductase 2] [gn:hmg2:l9324] [gtcf:3.4.8.1:8.2:12.16] [ec:1.1.1.34] [keggf:3.4] [sgdf:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4037	24220450_c3_5	3815	17918	1014	338	YLR450W	279	3.2(10)-23	Saccharomyces cerevisiae	[ui:ylr450w] [pn:3-hydroxy-3-methylglutaryl-coenzyme a reductase 2:hmg-coa reductase 2] [gn:hmg2:l9324] [gtcf:3.4.8.1:8.2:12.16] [ec:1.1.1.34] [keggf:3.4] [sgdf:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4037	10823550_c2_3	3816	17919	870	290	YLR450W	350	8.3(10)-31	Saccharomyces cerevisiae	[ui:ylr450w] [pn:3-hydroxy-3-methylglutaryl-coenzyme a reductase 2:hmg-coa reductase 2] [gn:hmg2:19324] [gtcf:3.4:8.1:8.2:12.16] [ec:1.1.1.34] [keggfc:3.4] [sgdfc:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1965	28242313_c3_5	3817	17920	402	134	YMR208W	164	1.6(10)-11	Saccharomyces cerevisiae	[ui:ymr208w] [pn:mevalonate kinase:mvk] [gn:rar1:erg12:ym8261] [gtcf:3.4:10.2] [ec:2.7.1.36] [keggfc:3.4] [sgdfc:1.6.4:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5199	22353426_fl_2	3818	17921	654	218	YMR208W	448	2.0(10)-42	Saccharomyces cerevisiae	[ui:ymr208w] [pn:mevalonate kinase:mvk] [gn:rar1:erg12:ym8261] [gtcf:3.4:10.2] [ec:2.7.1.36] [keggfc:3.4] [sgdfc:1.6.4:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2617	11177088_c3_7	3819	17922	1230	410	YMR220W	694	1.7(10)-68	Saccharomyces cerevisiae	[ui:ymr220w] [pn:phosphomevalonate kinase] [gn:erg8:ym9959] [gtcf:3.4:8.1:8.2] [ec:2.7.4.2] [keggfc:3.4] [sgdfc:1.6.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5378	9882002_c2_18	3820	17923	765	255	YMR220W	517	9.8(10)-50	Saccharomyces cerevisiae	[ui:ymr220w] [pn:phosphomevalonate kinase] [gn:erg8:ym9959] [gtcf:3.4:8.1:8.2] [ec:2.7.4.2] [keggfc:3.4] [sgdfc:1.6.1:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5601	20890782_f2_8	3821	17924	1050	350	YNR043W	1039	2.3(10)-110	Saccharomyces cerevisiae	[ui:ynr043w] [pn:diphosphomevalonate decarboxylase:mevalonate pyrophosphate decarboxylase] [gn:erg19:mvd1:mpd:n3427] [gtcf:3.4.8.1:8.2] [ec:4.1.1.33] [keggfc:3.4] [sgdgc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1153	25579387_c3_1	3822	17925	186	62	YPL117C	206	8.8(10)-17	Saccharomyces cerevisiae	[ui:ypl117c] [pn:isopentenyl-diphosphate delta-isomerase:ipp isomerase] [gn:idi1:boi2:iph10c] [gtcf:3.4.8.1:8.2:9.13] [ec:5.3.3.2] [keggfc:3.4:9.11] [sgdgc:1.6.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
b2x15112.y	24472625_f2_1	3823	17926	543	181	YPL117C	491	5.5(10)-47	Saccharomyces cerevisiae	[ui:ypl117c] [pn:isopentenyl-diphosphate delta-isomerase:ipp isomerase] [gn:idi1:boi2:iph10c] [gtcf:3.4.8.1:8.2:9.13] [ec:5.3.3.2] [keggfc:3.4:9.11] [sgdgc:1.6.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3968	35429566_f2_2	3824	17927	465	155	YAR044W	427	2.7(10)-39	Saccharomyces cerevisiae	[ui:yar044w] [pn:similarity to human oxysterol binding protein:osbp:osh1 protein] [gn:osh1:swl1] [gtcf:3.4.8.1:8.2:10.2] [keggfc:14.2] [sgdgc:1.6.1:4.8.3] [db:gtc-saccharomyces cerevisiae]

CONTIG1728	16509562_f1_1	3825	17928	693	231	YBR029C	635	3.1(10)-62	Saccharomyces cerevisiae	[ui:ybr029c] [pn:cdp-diacylglycerol synthase:phosphatidate cytidyltransferase:cdp-diglyceride synthetase:cdp-diglyceride pyrophosphorylase:cdp-diacylglycerol synthase] [gn:cdsl:cdgl:ybr0313] [gtcf:3.4:8.1:8.2:12.16] [ec:2.7.7.41]
CONTIG2244	10558385_c1_7	3826	17929	738	246	YBR029C	517	9.8(10)-50	Saccharomyces cerevisiae	[ui:ybr029c] [pn:cdp-diacylglycerol synthase:phosphatidate cytidyltransferase:cdp-diglyceride synthetase:cdp-diglyceride pyrophosphorylase:cdp-diacylglycerol synthase] [gn:cdsl:cdgl:ybr0313] [gtcf:3.4:8.1:8.2:12.16] [ec:2.7.7.41]
CONTIG3755	35413942_f2_2	3827	17930	270	90	YBR159W	225	1.1(10)-18	Saccharomyces cerevisiae	[ui:ybr159w] [pn:similarity to human 17-beta-hydroxysteroid dehydrogenase:hypothetical 38.7 kd protein in rpb5-cdc28 intergenic region] [gn:ybr1209] [gtcf:3.4:8.1:8.2] [keggfc:14.2] [sgdfc:1.6.1] [db:gtc-saccharomyces cerevisiae]

CONTIG1747	20117314_c1_2	3828	17931	675	225	YBR159W	633	5.0(10)-62	Saccharomyces cerevisiae	[ui:ybr159w] [pn:similarity to human 17-beta-hydroxysteroid dehydrogenase:hypothetical 38.7 kd protein in rpb5-cdc28 intergenic region] [gn:ybr1209] [gtcfc:3.4:8.1:8.2] [keggfc:14.2] [sgdgc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5601	22523251_c1_20	3829	17932	750	250	YDL142C	300	9.6(10)-27	Saccharomyces cerevisiae	[ui:ydl142c] [pn:phosphatidylglycerophosphate synthase] [gn:pgs1] [gtcfc:3.4:8.1:8.2] [keggfc:14.2] [sgdgc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4549	12140636_c1_7	3830	17933	942	314	YDL052C	654	3.0(10)-64	Saccharomyces cerevisiae	[ui:ydl052c] [pn:fatty acyltransferase:possible 1-acyl-sn-glycerol-3-phosphate acyltransferase] [gn:slc1] [gtcfc:3.4:8.1:8.2] [ec:2.3.1.51] [keggfc:8.1] [sgdgc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3968	35417136_f2_1	3831	17934	1254	418	YDL019C	927	3.5(10)-93	Saccharomyces cerevisiae	[ui:ydl019c] [pn:similarity to osh1p] [gtcfc:3.4:8.1:8.2] [keggfc:14.2] [sgdgc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4505	24344501_f2_3	3832	17935	2349	783	YDL019C	676	1.5(10)-75	Saccharomyces cerevisiae	[ui:ydl019c] [pn:similarity to osh1p] [gtcfc:3.4:8.1:8.2] [keggfc:14.2] [sgdgc:1.6.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5157	26798437_c3_10	3833	17936	369	123	YDR062W	252	7.7(10)-21	Saccharomyces cerevisiae	[ui:ydr062w] [pn:serine c-palmitoyltransferase subunit:serine base biosynthesis protein 2:spt 2] [gn:lcb2:scs1:yd9609] [gtcf:3.4.8.1:8.2:8.5] [ec:2.3.1.50] [keggfc:8.5] [sgdfe:1.6.1] [db:gtc-saccharo]
CONTIG5157	35173137_c2_6	3834	17937	936	312	YDR062W	1025	1.3(10)-103	Saccharomyces cerevisiae	[ui:ydr062w] [pn:serine c-palmitoyltransferase subunit:serine base biosynthesis protein 2:spt 2] [gn:lcb2:scs1:yd9609] [gtcf:3.4.8.1:8.2:8.5] [ec:2.3.1.50] [keggfc:8.5] [sgdfe:1.6.1] [db:gtc-saccharo]
CONTIG2898	15626_b3_2	3835	17938	336	112	YDR062W	187	8.4(10)-14	Saccharomyces cerevisiae	[ui:ydr062w] [pn:serine c-palmitoyltransferase subunit:serine base biosynthesis protein 2:spt 2] [gn:lcb2:scs1:yd9609] [gtcf:3.4.8.1:8.2:8.5] [ec:2.3.1.50] [keggfc:8.5] [sgdfe:1.6.1] [db:gtc-saccharo]

CONTIG887	19710752_c2_4	3836	17939	858	286	YDR208W	470	3.8(10)-44	Saccharomyces cerevisiae	[ui:ydr208w] [pn:similarity to human pip 5-kinase:probable phosphatidylinositol-4-phosphate 5-kinase mss4:1-phosphatidylinositol-4-phosphate kinase:pip5k:ptdins:4p-5-kinase:diphosphoinositide kinase] [gn:mss4:ydr8142a] [gtcfc:3.4.8.1:8
b9x12u09.x	50627_c1_1	3837	17940	582	194	YDR208W	446	1.7(10)-41	Saccharomyces cerevisiae	[ui:ydr208w] [pn:similarity to human pip 5-kinase:probable phosphatidylinositol-4-phosphate 5-kinase mss4:1-phosphatidylinositol-4-phosphate kinase:pip5k:ptdins:4p-5-kinase:diphosphoinositide kinase] [gn:mss4:ydr8142a] [gtcfc:3.4.8.1:8
CONTIG546	4038905_c2_4	3838	17941	1011	337	YGL126W	115	6.0(10)-15	Saccharomyces cerevisiae	[ui:ygl126w] [pn:inositol phospholipid synthesis protein:scs3 protein] [gn:scs3:g2868] [gtcfc:3.4.8.1:8.2] [keggfc:14.2] [sgdfc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1217	11117665_fl_1	3839	17942	726	242	YGL055W	283	2.2(10)-24	Saccharomyces cerevisiae	[ui:ygl055w] [pn:stearoyl-coa desaturase:acyl-coa desaturase 1:stearoyl-coa desaturase 1:fatty acid desaturase 1] [gn:ole1] [gtcfc:3.4.8.1:8.2:12.16] [ec:1.14.99.5] [keggfc:14.1] [sgdfc:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5698	4800011_f2_11	3840	17943	927	309	YGL055W	866	1.0(10)-86	Saccharomyces cerevisiae	[ui:yg055w] [pn:stearoyl-coa desaturase:acyl-coa desaturase 1:stearoyl-coa desaturase 1:fatty acid desaturase 1] [gn:ole1] [gtcf:3.4.8.1:8.2:12.16] [ec:1.14.99.5] [keggfc:14.1] [sgdfc:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5698	6642807_f1_1	3841	17944	381	127	YGL055W	304	1.1(10)-26	Saccharomyces cerevisiae	[ui:yg055w] [pn:stearoyl-coa desaturase:acyl-coa desaturase 1:stearoyl-coa desaturase 1:fatty acid desaturase 1] [gn:ole1] [gtcf:3.4.8.1:8.2:12.16] [ec:1.14.99.5] [keggfc:14.1] [sgdfc:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG506	204700_f1_2	3842	17945	795	265	YGL012W	802	6.2(10)-80	Saccharomyces cerevisiae	[ui:yg012w] [pn:sterol c-24 reductase:c-24:28 sterol reductase] [gn:erg4:yg1022] [gtcf:3.4.8.1:8.2] [ec:1.-.-.-] [keggfc:14.1] [sgdfc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4272	31336678_f2_2	3843	17946	903	301	YGL001C	1083	1.0(10)-109	Saccharomyces cerevisiae	[ui:yg001c] [pn:putative 3-beta-hydroxysteroid dehydrogenase:putative 3-beta dehydroxy-5-ene steroid dehydrogenase / steroid delta-isomerase:3beta-hsd:progesterone reductase] [gtcf:3.4.3.6:3.7.8.1:8.2] [keggfc:3.6:3.7] [sgdfc:1.6.1] [

CONTIG5167	22063392_c3_16	3844	17947	648	216	YGR007W	391	2.2(10)-36	Saccharomyces cerevisiae	[ui:ygr007w] [pn:choline phosphate cytidyltransferase:protein] [gn:muq1] [gdcfc:3.4.8.1:8.2] [keggfc:14.2] [sgdgc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3381	12506943_c2_2	3845	17948	960	320	YGR037C	122	2.6(10)-7	Saccharomyces cerevisiae	[ui:ygr037c] [pn:acyl-coenzyme-a-binding protein:diazepam binding inhibitor:acyl-coa-binding protein:acbp] [gn:acbl:acb] [gdcfc:3.4.8.1:8.2:12.2] [keggfc:14.2] [sgdgc:1.6.1:1.6.5] [db:gtc-saccharomyces cerevisiae]
CONTIG4951	6814008_fl_1	3846	17949	234	78	YGR037C	270	1.5(10)-23	Saccharomyces cerevisiae	[ui:ygr037c] [pn:acyl-coenzyme-a-binding protein:diazepam binding inhibitor:acyl-coa-binding protein:acbp] [gn:acbl:acb] [gdcfc:3.4.8.1:8.2:12.2] [keggfc:14.2] [sgdgc:1.6.1:1.6.5] [db:gtc-saccharomyces cerevisiae]
CONTIG1332	953392_c3_3	3847	17950	921	307	YGR060W	834	1.8(10)-85	Saccharomyces cerevisiae	[ui:ygr060w] [pn:c-4 sterol methyl oxidase:c-4 methyl sterol oxidase] [gn:erg25:fet6] [gdcfc:3.4.8.1:8.2:12.16] [ec:1---] [keggfc:14.1] [sgdgc:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4151	6853437_f2_2	3848	17951	969	323	YGR060W	910	2.2(10)-91	Saccharomyces cerevisiae	[ui:ygr060w] [pn:c-4 sterol methyl oxidase:c-4 methyl sterol oxidase] [gn:erg25:fet6] [gdcfc:3.4.8.1:8.2:12.16] [ec:1---] [keggfc:14.1] [sgdgc:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3701	4375802_c2_5	3849	17952	318	106	YGR060W	246	5.0(10)-21	Saccharomyces cerevisiae	[ui:ygr060w] [pn:c-4 sterol methyl oxidase:c-4 methyl sterol oxidase] [gn:erg25:fet6] [gtcf:3.4:8.1:8.2:12.16] [ec:1.-.-] [keggf:1.4.1] [sgdfc:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1185	23495718_c2_2	3850	17953	660	220	YGR157W	123	3.0(10)-13	Saccharomyces cerevisiae	[ui:ygr157w] [pn:phosphatidylethanolamine n-methyltransferase] [gn:pem1:cho2:g6673] [gtcf:3.4:5.3:8.1:8.2:12.16] [ec:2.1.1.17] [keggf:5.3] [sgdfc:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3467	171877_c3_5	3851	17954	672	224	YGR157W	199	8.8(10)-15	Saccharomyces cerevisiae	[ui:ygr157w] [pn:phosphatidylethanolamine n-methyltransferase] [gn:pem1:cho2:g6673] [gtcf:3.4:5.3:8.1:8.2:12.16] [ec:2.1.1.17] [keggf:5.3] [sgdfc:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5637	34492200_f3_7	3852	17955	1116	372	YGR170W	596	4.0(10)-57	Saccharomyces cerevisiae	[ui:ygr170w] [pn:phosphatidylserine decarboxylase 2:phosphatidylserine precursor] [gn:psd2] [gtcf:3.4:5.3:8.1:8.2:12.16] [ec:4.1.1.65] [keggf:5.3:8.1] [sgdfc:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5637	36064812_fl_1	3853	17956	720	240	YGR170W	531	4.0(10)-50	Saccharomyces cerevisiae	[ui:ygr170w] [pn:phosphatidylserine decarboxylase 2:phosphatidylserine precursor] [gn:psd2] [gtcf:3.4.5.3.8.1:8.2:12.16] [ec:4.1.1.65] [keggf:5.3.8.1] [sgdf:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]
b2x18670.x	2401038_f2_1	3854	17957	576	192	YGR170W	290	2.5(10)-24	Saccharomyces cerevisiae	[ui:ygr170w] [pn:phosphatidylserine decarboxylase 2:phosphatidylserine precursor] [gn:psd2] [gtcf:3.4.5.3.8.1:8.2:12.16] [ec:4.1.1.65] [keggf:5.3.8.1] [sgdf:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5670	33337762_fl_5	3855	17958	1377	459	YGR202C	957	2.2(10)-96	Saccharomyces cerevisiae	[ui:ygr202c] [pn:cholinephosphate cytidylyltransferase:phosphorylcholine transferase:ct] [gn:pct1:cct1:cct:g7729] [gtcf:3.4.6.3.8.1:8.2:12.16] [ec:2.7.7.15] [keggf:6.3.8.1] [sgdf:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3973	156567_f2_3	3856	17959	1455	485	YGR216C	287	4.9(10)-32	Saccharomyces cerevisiae	[ui:ygr216c] [pn:required for n-acetylglucosaminyl phosphatidylinositol synthesis:hypothetical 70.4 kd protein in nab1a-crm1 intergenic region] [gn:gpi1] [gtcf:3.4:8.1:8.2] [keggf:14.2] [sgdfc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG130	17033563_c1_4	3857	17960	534	178	YHR001W	486	1.8(10)-46	Saccharomyces cerevisiae	[ui:yhr001w] [pn:similarity to kes1p:hypothetical 49.8 kd protein in rpl14b-gpa1 intergenic region] [gtcf:3.4:8.1:8.2:8.5] [keggf:14.2] [sgdfc:1.6.1:1.6.6] [db:gtc-saccharomyces cerevisiae]
CONTIG56	1723200_f2_1	3858	17961	642	214	YHR001W	535	1.2(10)-51	Saccharomyces cerevisiae	[ui:yhr001w] [pn:similarity to kes1p:hypothetical 49.8 kd protein in rpl14b-gpa1 intergenic region] [gtcf:3.4:8.1:8.2:8.5] [keggf:14.2] [sgdfc:1.6.1:1.6.6] [db:gtc-saccharomyces cerevisiae]
CONTIG5249	14665887_f2_1	3859	17962	2538	846	YHR073W	982	4.0(10)-136	Saccharomyces cerevisiae	[ui:yhr073w] [pn:similarity to osh1p, ydl019c and mammalian oxysterol-binding protei:hypothetical 113.8 kd protein in erg7-nmd2 intergenic region] [gtcf:3.4:8.1:8.2] [keggf:14.2] [sgdfc:1.6.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5694	14250878_c2_21	3860	17963	699	233	YIR035C	570	2.3(10)-55	Saccharomyces cerevisiae	[ui:yir035c] [pn:similarity to human corticosteroid 11-beta-dehydrogenase:hypothetical oxidoreductase in lys1-hyr1 intergenic region] [gtcf:3.4.8.1:8.2] [ec:1.-.-.] [keggf:14.1] [sgdf:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5694	51342_c1_18	3861	17964	798	266	YIR035C	540	3.6(10)-52	Saccharomyces cerevisiae	[ui:yir035c] [pn:similarity to human corticosteroid 11-beta-dehydrogenase:hypothetical oxidoreductase in lys1-hyr1 intergenic region] [gtcf:3.4.8.1:8.2] [ec:1.-.-.] [keggf:14.1] [sgdf:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3615	23600262_fl_1	3862	17965	1218	406	YJL196C	177	2.5(10)-11	Saccharomyces cerevisiae	[ui:yjl196c] [pn:fatty acid elongation protein:hypothetical 36.2 kd protein in ubp12-cdc6 intergenic region] [gn:elo1:j0343] [gtcf:3.4.8.1:8.2] [keggf:14.2] [sgdf:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4808	2767125_c1_8	3863	17966	318	106	YJR073C	222	1.8(10)-18	Saccharomyces cerevisiae	[ui:yjr073c] [pn:methylene-fatty-acyl-phospholipid synthase:unsaturated phospholipid methyltransferase] [gn:pem2:opi3:j1824] [gtcf:3.4.8.1:8.2:12.16] [ec:2.1.1.16] [keggf:14.1] [sgdf:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1917	16972215_c1_5	3864	17967	1014	338	YKL203C	1241	4.4(10)-125	Saccharomyces cerevisiae	[ui:ykl203c] [pn:phosphatidylinositol 3-kinase:phosphatidylinositol 3-kinase:phosphatidylinositol 3-kinase:pi3k] [gn:tor2:drp2] [gtfc:3.4.8.1:8.2:12.8] [ec:2.7.1.137] [keggc:8.1] [sgdfc:1.6.1.3.1.0.3.8.0] [db:gtc-saccharomyces cer
CONTIG58	35167202_c1_1	3865	17968	852	284	YKL203C	778	9.0(10)-76	Saccharomyces cerevisiae	[ui:ykl203c] [pn:phosphatidylinositol 3-kinase:phosphatidylinositol 3-kinase:phosphatidylinositol 3-kinase:pi3k] [gn:tor2:drp2] [gtfc:3.4.8.1:8.2:12.8] [ec:2.7.1.137] [keggc:8.1] [sgdfc:1.6.1.3.1.0.3.8.0] [db:gtc-saccharomyces cer
CONTIG869	16494055_c3_2	3866	17969	552	184	YKL203C	311	4.0(10)-26	Saccharomyces cerevisiae	[ui:ykl203c] [pn:phosphatidylinositol 3-kinase:phosphatidylinositol 3-kinase:phosphatidylinositol 3-kinase:pi3k] [gn:tor2:drp2] [gtfc:3.4.8.1:8.2:12.8] [ec:2.7.1.137] [keggc:8.1] [sgdfc:1.6.1.3.1.0.3.8.0] [db:gtc-saccharomyces cer

b9x10w65.y	31413532_f1_1	3867	17970	606	202	YKL203C	775	1.8(10)-75	Saccharomyces cerevisiae	[ui:ykl203c] [pn:phosphatidylinositol 3-kinase:phosphatidylinositol 3-kinase:pi3-kinase:ptdins-3-kinase:pi3k] [gn:tor2:dnr2] [gtcf:3.4.8.1:8.2:12.8] [ec:2.7.1.137] [keggf:8.1] [sgdfc:1.6.1:3.1.0:3.8.0] [db:gtc-saccharomyces cer
CONTIG2802	21906312_f1_1	3868	17971	1083	361	YKR003W	956	3.0(10)-96	Saccharomyces cerevisiae	[ui:ykr003w] [pn:similarity to kes1p, hes1p and osh1p:hypothetical 51.6 kd protein in pap1-mrp113 intergenic region] [gn:yk102] [gtcf:3.4.8.1:8.2] [keggf:14.2] [sgdfc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2802	14665632_f3_3	3869	17972	327	109	YKR003W	244	2.8(10)-20	Saccharomyces cerevisiae	[ui:ykr003w] [pn:similarity to kes1p, hes1p and osh1p:hypothetical 51.6 kd protein in pap1-mrp113 intergenic region] [gn:yk102] [gtcf:3.4.8.1:8.2] [keggf:14.2] [sgdfc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3959	85753_f3_5	3870	17973	1122	374	YLR056W	879	1.2(10)-93	Saccharomyces cerevisiae	[ui:ylr056w] [pn:c-5 sterol desaturase] [gn:erg3:syr1:12150] [gtcf:3.4.8.1:8.2:12.16] [ec:1.-.-.] [keggf:14.1] [sgdfc:1.6.1:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5660	14953268_f2_9	3871	17974	1926	642	YLR133W	648	6.2(10)-72	Saccharomyces cerevisiae	[ui:ylr133w] [pn:choline kinase] [gn:ck1:cki1:13130:19606] [gtcf:3.4.8.1:8.2] [ec:2.7.1.32] [keggf:8.1] [sgdfc:1.6.1:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5233	506262_c1_8	3872	17975	969	323	YML131W	460	1.1(10)-43	Saccharomyces cerevisiae	[ui:ym131w] [pn:similarity to human leukotriene b4 12-hydroxydehydrogenase] [gicfc:3.4:8.1:8.2] [keggfc:14.2] [sgdgc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3880	23609675_f1_1	3873	17976	1164	388	YML008C	1288	1.8(10)-131	Saccharomyces cerevisiae	[ui:ym1008c] [pn:s-adenosyl-methionine delta-24-sterol-c-methyltransferase] [gn:erg6:sed6:ise1:isl:ym9571] [gicfc:3.4:8.1:8.2] [ec:2.1.1.41] [keggfc:14.1] [sgdgc:1.6.1] [db:gtc-saccharomyces cerev]
CONTIG1458	1055313_f1_1	3874	17977	840	280	YMR296C	462	6.5(10)-44	Saccharomyces cerevisiae	[ui:ymr296c] [pn:serine c-palmitoyltransferase subunit:serine palmitoyltransferase 1:long chain base biosynthesis protein 1:spt 1] [gn:lcb1] [gicfc:3.4:8.1:8.2:8.5] [ec:2.3.1.50] [keggfc:8.5] [sgdgc:1.6.1] [db:gtc-saccharomyces cerevi]
CONTIG3044	24647501_f2_3	3875	17978	534	178	YNL280C	270	3.1(10)-23	Saccharomyces cerevisiae	[ui:ynl280c] [pn:c-14 sterol reductase] [gn:erg24:n0593] [gicfc:3.4:8.1:8.2] [ec:1.-.-.] [keggfc:14.1] [sgdgc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1381	242010_f2_3	3876	17979	726	242	YNL111C	191	3.3(10)-15	Saccharomyces cerevisiae	[ui:ynl111c] [pn:cytochrome b5] [gn:cyb5:n1949] [gicfc:3.4:8.1:8.2] [keggfc:14.2] [sgdgc:1.6.1] [db:gtc-saccharomyces cerevisiae]

CONTIG3299	12995686_f3_2	3877	17980	1290	430	YNL045W	1010	5.5(10)-102	Saccharomyces cerevisiae	[ui:ynl045w] [pn:strong similarity to human leukotriene-a4 hydrolase:probable leukotriene a-4 hydrolase:Ita-4 hydrolase:leukotriene a:4 hydrolase] [gn:n2535] [gtcf:3.4.8.1:8.2] [ec:3.3.2.6] [keggf:8.6] [sgdf:1.6.1] [db:gtc-saccharo]
CONTIG3906	13953535_f2_5	3878	17981	357	119	YNL045W	135	4.2(10)-8	Saccharomyces cerevisiae	[ui:ynl045w] [pn:strong similarity to human leukotriene-a4 hydrolase:probable leukotriene a-4 hydrolase:Ita-4 hydrolase:leukotriene a:4 hydrolase] [gn:n2535] [gtcf:3.4.8.1:8.2] [ec:3.3.2.6] [keggf:8.6] [sgdf:1.6.1] [db:gtc-saccharo]
CONTIG4024	26432750_c3_6	3879	17982	1260	420	YNR019W	677	3.5(10)-92	Saccharomyces cerevisiae	[ui:ynr019w] [pn:acyl-coa sterol acyltransferase 2:sterol-ester synthase 2] [gn:are2:sat1:n3206] [gtcf:3.4.3.5:8.1:8.2:12.1:5] [ec:2.3.1.26] [keggf:3.5] [sgdf:1.6.1:3.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5797	10582762_c3_30	3880	17983	1335	445	YPL145C	1191	3.7(10)-121	Saccharomyces cerevisiae	[ui:yp145c] [pn:involved in ergosterol biosynthesis:kes1 protein] [gn:kes1:lpi3c:p2614] [gtcf:3.4.8.1:8.2:12.1:0] [keggf:14.2] [sgdf:1.6.1:8.3.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5810	4407203_c3_36	3881	17984	798	266	YPL076W	251	1.5(10)-21	Saccharomyces cerevisiae	[ui:yp1076w] [pn:n-acetylglucosaminyl-phosphatidylinositol biosynthetic protein:n-acetylglucosaminyl-phosphatidylinositol biosynthetic protein gpi2] [gn:gpi2:gc4:lp19w] [gtcfc:3.4.8.1:8.2] [keggfc:14.2] [sgdgc:1.6.1] [db:gtc-saccharo
CONTIG2518	20586442_f2_2	3882	17985	498	166	YPL069C	223	1.3(10)-18	Saccharomyces cerevisiae	[ui:yp1069c] [pn:geranylgeranyl diphosphate synthase] [gn:bs1] [gtcfc:3.4.8.1:8.2] [keggfc:14.2] [sgdgc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4222	20578786_c2_13	3883	17986	486	162	YPL069C	148	5.0(10)-10	Saccharomyces cerevisiae	[ui:yp1069c] [pn:geranylgeranyl diphosphate synthase] [gn:bs1] [gtcfc:3.4.8.1:8.2] [keggfc:14.2] [sgdgc:1.6.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3382	14097510_f3_4	3884	17987	747	249	YPR113W	550	3.1(10)-53	Saccharomyces cerevisiae	[ui:ypr113w] [pn:cdp diacylglycerol--inositol 3-phosphatidyltransferase:cdp-diacylglycerol--inositol 3-phosphatidyltransferase:phosphatidylinositol synthase] [gn:pis1:pis:p8283] [gtcfc:3.4.8.1:8.2:12.16] [ec:2.7.8.1] [keggfc:8.1] [s
CONTIG4607	26204657_f1_1	3885	17988	456	152	YBR034C	601	1.2(10)-58	Saccharomyces cerevisiae	[ui:ybr034c] [pn:hmrp methyltransferase:hmrp arginine n-methyltransferase:odp1 protein] [gn:hmt1:odp1:rmt1:ybr0320] [gtcfc:3.7.5.11:5.14:9.12:10.1:10.2:10.7] [ec:2.1.1.-] [keggfc:3.7.5.11:5.14:9.13] [sgdgc:6.3.0:9.5.0] [db:gtc-sacch

CONTIG4607	26441635_f1_2	3886	17989	591	197	YBR034C	506	1.3(10)-48	Saccharomyces cerevisiae	[ui:ybr034c] [pn:hmrp methyltransferase:odp1 protein] [gn:hmt1:odp1:rmt1:ybr0320] [gtrfc:3.7:5.11:5.14:9.12:10.1:10.2:10.7] [ec:2.1.1.-] [keggfc:3.7:5.11:5.14:9.13] [sgdfc:6.3.0:9.5.0] [db:gtr-sacch
CONTIG5565	23848387_f2_6	3887	17990	999	333	YPL266W	1320	7.9(10)-135	Saccharomyces cerevisiae	[ui:ypl266w] [pn:rma:adenine-n6,n6-- dimethyltransferase:dimethyladenosine transferase:s-adenosylmethionine-6-n", n"-adenosyl:rma dimethyltransferase:18s rma dimethylase] [gn:dim1] [gtrfc:3.7:5.11:5.14:9.12:10.1:10.2:10.3] [ec:2.1.1
CONTIG2392	21989575_c1_2	3888	17991	948	316	YAR015W	931	1.3(10)-93	Saccharomyces cerevisiae	[ui:yar015w] [pn:phosphoribosylamidoimidazole-succinocarboxamide synthase:saicar synthetase] [gn:ade1] [gtrfc:4.1] [ec:6.3.2.6] [keggfc:4.1] [sgdfc:1.3.1] [db:gtr-saccharomyces cerevisiae]
CONTIG5717	196076_c2_15	3889	17992	393	131	YDL150W	147	1.1(10)-9	Saccharomyces cerevisiae	[ui:ydl150w] [pn:dna-directed rna polymerase iii, 47 kd subunit:dna-directed rna polymerase iii 47 kd polypeptide:c53:rma polymerase c subunit 4] [gn:rpc4:rpc53:d1557] [gtrfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdf

CONTIG2231	2507812_f2_1	3890	17993	771	257	YDL140C	904	1.5(10)-89	Saccharomyces cerevisiae	[ui:yd1140c] [pn:dna-directed ma polymerase ii, 215 kd subunit:dna-directed rna polymerase ii largest subunit:b220] [gn:rpb1:rpo21:rpb220:sua8:d2150] [gtcf:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.8.1:9.5.0] [db:gtc]
CONTIG2835	11761285_c3_10	3891	17994	1116	372	YDL140C	1462	7.0(10)-150	Saccharomyces cerevisiae	[ui:yd1140c] [pn:dna-directed ma polymerase ii, 215 kd subunit:dna-directed rna polymerase ii largest subunit:b220] [gn:rpb1:rpo21:rpb220:sua8:d2150] [gtcf:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.8.1:9.5.0] [db:gtc]
CONTIG2835	22662842_c3_9	3892	17995	735	245	YDL140C	1099	1.5(10)-110	Saccharomyces cerevisiae	[ui:yd1140c] [pn:dna-directed ma polymerase ii, 215 kd subunit:dna-directed rna polymerase ii largest subunit:b220] [gn:rpb1:rpo21:rpb220:sua8:d2150] [gtcf:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.8.1:9.5.0] [db:gtc]
CONTIG5417	31683333_f3_6	3893	17996	1341	447	YDL140C	669	1.8(10)-64	Saccharomyces cerevisiae	[ui:yd1140c] [pn:dna-directed ma polymerase ii, 215 kd subunit:dna-directed rna polymerase ii largest subunit:b220] [gn:rpb1:rpo21:rpb220:sua8:d2150] [gtcf:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.8.1:9.5.0] [db:gtc]

CONTIG810	10833318_f1_1	3894	17997	732	244	YDL140C	769	4.0(10)-75	Saccharomyces cerevisiae	[ui:ydl140c] [pn:dna-directed dna polymerase ii, 215 kd subunit:dna-directed rna polymerase ii largest subunit:b220] [gn:rpbl:rho21:rbp220:uaa8:d2150] [gtcf:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.8.1:9.5.0] [db:gtc]
CONTIG4028	2347026_f1_1	3895	17998	2163	721	YDL102W	2301	8.8(10)-239	Saccharomyces cerevisiae	[ui:ydl102w] [pn:dna-directed dna polymerase delta, catalytic 125 kd subunit:dna polymerase delta large chain:dna polymerase iii] [gn:pol3:cdc2:tex1:d2366] [gtcf:4.1:4.2:10.1:10.10.2:10.8:12.8] [ec:2.7.7.7] [keggfc:4.1:4.2:13.3] [
CONTIG5053	33787811_f2_4	3896	17999	480	160	YDR156W	90	0.003	Saccharomyces cerevisiae	[ui:ydr156w] [pn:dna-directed dna polymerase i, alpha 4 subunit:dna-directed rna polymerase i 14 kd polypeptide:alpha 4] [gn:rpai4:ydr8358] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:9.5.0] [db:gtc-saccharomyces
CONTIG3853	1214525_c3_7	3897	18000	675	225	YDR226W	826	1.8(10)-82	Saccharomyces cerevisiae	[ui:ydr226w] [pn:adenylate kinase, cytosolic:adenylate kinase cytosolic:atp- amp transphosphorylase] [gn:adkl:aky1:aky2:ydr9934] [gtcf:4.1:12.13] [ec:2.7.4.3] [keggfc:4.1] [sgdfc:1.3.8:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2602	24792827_c1_4	3898	18001	819	273	YDR408C	483	3.8(10)-46	Saccharomyces cerevisiae	[ui:ydr408c] [pn:phosphoribosylglycinamide formyltransferase:gart:gar transformylase:5"-phosphoribosylglycinamide transformylase] [gn:ade8:d9509] [gtcf:4.1:9.6] [ec:2.1.2.2] [keggf:4.1:9.8] [sgdfc:1.3.1:9.2.0] [db:gtc-saccharomyces]
CONTIG2638	33204635_c2_5	3899	18002	411	137	YDR454C	495	2.1(10)-47	Saccharomyces cerevisiae	[ui:ydr454c] [pn:guanylate kinase:gmp kinase] [gn:guk1:d9461] [gtcf:4.1:12.13] [ec:2.7.4.8] [keggf:4.1] [sgdfc:1.3.8] [db:gtc-saccharomyces cerevisiae]
CONTIG1452	16302268_fl_1	3900	18003	948	316	YDR530C	266	4.9(10)-31	Saccharomyces cerevisiae	[ui:ydr530c] [pn:atp adenyllyltransferase ii:5"-p-4-tetraphosphate phosphorylase ii:ap-4-a phosphorylase ii:atp adenyllyltransferase:ap,a phosphorylase ii] [gn:apa2:d9719] [gtcf:4.1] [ec:2.7.7.53] [keggf:4.1] [sgdfc:1.3.4] [d
CONTIG5136	78130_c2_7	3901	18004	2661	887	YER070W	3253	0	Saccharomyces cerevisiae	[ui:yer070w] [pn:ribonucleoside-diphosphate reductase, large subunit:ribonucleoside-diphosphate reductase large chain 1:ribonucleotide reductase] [gn:mr1] [gtcf:4.1:4.2:10.8:12.8] [ec:1.17.4.1] [keggf:4.1:4.2:13.2] [sgdfc:1.3.3:3.6

CONTIG5807	10548267_f2_2	3902	18005	2253	751	YER070W	2376	2.6(10)-252	Saccharomyces cerevisiae	[ui:yer070w] [pn:ribonucleoside-diphosphate reductase, large subunit:ribonucleoside-diphosphate reductase large chain l:ribonucleotide reductase] [gn:mr1] [gtcf:4.1:4.2:10.8:12.8] [ec:1.17.4.1] [keggfc:4.1:4.2:13.2] [sgdfc:1.3:3.6]
CONTIG5743	2148252_f1_6	3903	18006	2493	831	YGL234W	2569	3.5(10)-267	Saccharomyces cerevisiae	[ui:ygl234w] [pn:phosphoribosylamine-glycine ligase and phosphoribosylformylglycinamide cyclo-ligase] [gn:ade5:7] [gtcf:4.1] [keggfc:4.1] [sgdfc:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4022	10193966_c3_4	3904	18007	432	144	YGL070C	383	1.5(10)-35	Saccharomyces cerevisiae	[ui:ygl070c] [pn:dna-directed m polymerase ii, 14.2 kd subunit:dna-directed m polymerase ii 14.2 kd polypeptide:b12.6] [gn:rpb9] [gtcf:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces cer
CONTIG2815	21876_c3_1	3905	18008	1512	504	YGR061C	1316	2.1(10)-134	Saccharomyces cerevisiae	[ui:ygr061c] [pn:5"-phosphoribosylformylglycinamide synthetase:phosphoribosylformylglycinamide synthase:fgam synthase:formylglycineamide ribotide amidotransferase:fgarat] [gn:ade6] [gtcf:4.1] [ec:6.3.5.3] [keggfc:4.1] [sgdfc:1.3

CONTIG5777	12947078_c1_18	3906	18009	618	206	YGR061C	552	3.5(10)-52	Saccharomyces cerevisiae	[ui:ygr061c] [pn:5"-phosphoribosylformylglycinamide synthetase:phosphoribosylformylglycinamide synthase:fgam synthase:formylglycineamide ribotide amidotransferase:fgarat] [gn:ade6] [gtcf:4.1] [ec:6.3.5.3] [keggfc:4.1] [sgdfc:1.3]
CONTIG5777	16672192_c3_25	3907	18010	660	220	YGR061C	712	2.5(10)-69	Saccharomyces cerevisiae	[ui:ygr061c] [pn:5"-phosphoribosylformylglycinamide synthetase:phosphoribosylformylglycinamide synthase:fgam synthase:formylglycineamide ribotide amidotransferase:fgarat] [gn:ade6] [gtcf:4.1] [ec:6.3.5.3] [keggfc:4.1] [sgdfc:1.3]
CONTIG5777	17087514_c1_16	3908	18011	1155	385	YGR061C	1294	4.5(10)-132	Saccharomyces cerevisiae	[ui:ygr061c] [pn:5"-phosphoribosylformylglycinamide synthetase:phosphoribosylformylglycinamide synthase:fgam synthase:formylglycineamide ribotide amidotransferase:fgarat] [gn:ade6] [gtcf:4.1] [ec:6.3.5.3] [keggfc:4.1] [sgdfc:1.3]
CONTIG2819	7120275_c2_2	3909	18012	897	299	YHR201C	293	2.3(10)-31	Saccharomyces cerevisiae	[ui:yhr201c] [pn:exopolyphosphate:metaphosphatase] [gn:ppx1] [gtcf:4.1:13.10] [ec:3.6.1.1] [keggfc:4.1] [sgdfc:1.4.1:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5807	5078401_f3_6	3910	18013	285	95	YIL066C	95	0.00119	Saccharomyces cerevisiae	[ui:yil066c] [pn:ribonucleotide reductase, repair inducible large subunit:ribonucleoside-diphosphate reductase large chain 2:ribonucleotide reductase:ribonucleotide reductase dna damage- inducible regulatory subunit] [gn:mr3:din1] [gt
CONTIG1887	14648437_fl_2	3911	18014	456	152	YIL021W	343	2.7(10)-31	Saccharomyces cerevisiae	[ui:yil021w] [pn:dna-directed rna polymerase ii, 45 kda:dna-directed rna polymerase ii 45 kd polypeptide:b44.5] [gn:rpbb3] [gtcf:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggf:4.1:4.2] [sgdf:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5137	24414062_cl_9	3912	18015	1074	358	YIL021W	896	6.7(10)-90	Saccharomyces cerevisiae	[ui:yil021w] [pn:dna-directed rna polymerase ii, 45 kda:dna-directed rna polymerase ii 45 kd polypeptide:b44.5] [gn:rpbb3] [gtcf:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggf:4.1:4.2] [sgdf:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2481	36111703_f3_3	3913	18016	549	183	YJL140W	194	1.6(10)-15	Saccharomyces cerevisiae	[ui:yjl140w] [pn:dna-directed rna polymerase ii, 32 kda subunit:dna-directed rna polymerase ii 32 kd polypeptide:b32] [gn:rpbb4:j0654] [gtcf:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggf:4.1:4.2] [sgdf:4.8.1:9.5.0] [db:gtc-saccharomyces ce

CONTIG5239	14640628_fl_1	3914	18017	1236	412	YJL026W	1401	2.1(10)-143	Saccharomyces cerevisiae	[ui:yj1026w] [pn:ribonucleoside-diphosphate reductase, small subunit:ribonucleoside-diphosphate reductase small chain 1:ribonucleotide reductase] [gn:mr2:j1271] [gcf:4.1:4.2:10.8] [ec:1.17.4.1] [keggfc:4.1:4.2] [sgdfe:1.3.3:3.6.0]
CONTIG5714	22381317_c2_20	3915	18018	1083	361	YJL026W	1149	1.0(10)-116	Saccharomyces cerevisiae	[ui:yj1026w] [pn:ribonucleoside-diphosphate reductase, small subunit:ribonucleoside-diphosphate reductase small chain 1:ribonucleotide reductase] [gn:mr2:j1271] [gcf:4.1:4.2:10.8] [ec:1.17.4.1] [keggfc:4.1:4.2] [sgdfe:1.3.3:3.6.0]
CONTIG2234	21678181_c2_6	3916	18019	1059	353	YJL005W	97	0.20999	Saccharomyces cerevisiae	[ui:yj1005w] [pn:adenylate cyclase:atp pyrophosphate-lyase:adenylate cyclase] [gn:cyr1:cdc35:hsr1:sra4:j1401] [gcf:4.1:1.1:1.12.13:12.8] [ec:4.6.1.1] [keggfc:4.1:13.1] [sgdfe:1.3.4:3.8.0:9.1.0:10.4.3] [db:gtc-saccharomyces cerevisiae]
CONTIG3421	24323555_c1_7	3917	18020	2085	695	YJL005W	1216	9.4(10)-123	Saccharomyces cerevisiae	[ui:yj1005w] [pn:adenylate cyclase:atp pyrophosphate-lyase:adenylate cyclase] [gn:cyr1:cdc35:hsr1:sra4:j1401] [gcf:4.1:1.1:1.12.13:12.8] [ec:4.6.1.1] [keggfc:4.1:13.1] [sgdfe:1.3.4:3.8.0:9.1.0:10.4.3] [db:gtc-saccharomyces cerevisiae]

CONTIG3985	14117003_f3_7	3918	18021	705	235	YJL005W	377	3.0(10)-33	Saccharomyces cerevisiae	[ui:yj1005w] [pn:adenylate cyclase:atp pyrophosphate-lyase:adenylate cyclase] [gn:cyr1:cdc35:hsr1:sra4:j1401] [gtcf:4.1:11.1:12.13:12.8] [ec:4.6.1.1] [keggfc:4.1:13.1] [sgdfc:1.3.4:3.8.0:9.1.0:10.4.3] [db:gtc-saccharomyces cerevisiae]
CONTIG4866	23531307_f2_3	3919	18022	1272	424	YJL005W	146	2.2(10)-6	Saccharomyces cerevisiae	[ui:yj1005w] [pn:adenylate cyclase:atp pyrophosphate-lyase:adenylate cyclase] [gn:cyr1:cdc35:hsr1:sra4:j1401] [gtcf:4.1:11.1:12.13:12.8] [ec:4.6.1.1] [keggfc:4.1:13.1] [sgdfc:1.3.4:3.8.0:9.1.0:10.4.3] [db:gtc-saccharomyces cerevisiae]
CONTIG5507	3960080_f2_5	3920	18023	1902	634	YJL005W	127	0.00044	Saccharomyces cerevisiae	[ui:yj1005w] [pn:adenylate cyclase:atp pyrophosphate-lyase:adenylate cyclase] [gn:cyr1:cdc35:hsr1:sra4:j1401] [gtcf:4.1:11.1:12.13:12.8] [ec:4.6.1.1] [keggfc:4.1:13.1] [sgdfc:1.3.4:3.8.0:9.1.0:10.4.3] [db:gtc-saccharomyces cerevisiae]
CONTIG5692	21650260_f1_1	3921	18024	777	259	YJL005W	102	0.042	Saccharomyces cerevisiae	[ui:yj1005w] [pn:adenylate cyclase:atp pyrophosphate-lyase:adenylate cyclase] [gn:cyr1:cdc35:hsr1:sra4:j1401] [gtcf:4.1:11.1:12.13:12.8] [ec:4.6.1.1] [keggfc:4.1:13.1] [sgdfc:1.3.4:3.8.0:9.1.0:10.4.3] [db:gtc-saccharomyces cerevisiae]

CONTIG88	26690930_f3_2	3922	18025	609	203	YJL005W	188	3.7(10)-13	Saccharomyces cerevisiae	[ui:yjl005w] [pn:adenylate cyclase:atp pyrophosphatase:adenylate cyclase] [gn:cyr1:cdc35:hsr1:sra4:j1401] [gtcf:4.1:1.1:12.13:12.8] [ec:4.6.1.1] [keggf:4.1:13.1] [sgdf:1.3.4.3.8.0.9.1.0:10.4.3] [db:gtc-saccharomyces cerevisiae]
CONTIG5230	4490806_f2_11	3923	18026	381	127	YJR063W	481	6.4(10)-46	Saccharomyces cerevisiae	[ui:yjr063w] [pn:dna-directed rna polymerase i, 13.7 kd subunit:dna-directed rna polymerase i 13.7 kd polypeptide:a12.2] [gn:tpa12:rm4:j1747] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggf:4.1:4.2] [sgdf:4.1.0:9.5.0] [db:gtc-sa
CONTIG5131	31447187_cl_4	3924	18027	1098	366	YJR105W	735	7.7(10)-73	Saccharomyces cerevisiae	[ui:yjr105w] [pn:strong similarity to human adenosine kinase:putative adenosine kinase] [gn:j1973] [gtcf:4.1] [ec:2.7.1.20] [keggf:4.1] [sgdf:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3012	5863775_fl_1	3925	18028	519	173	YKL144C	476	2.2(10)-45	Saccharomyces cerevisiae	[ui:ykl144c] [pn:dna-directed rna polymerase iii, 25 kd subunit:dna-directed rna polymerase iii 25 kd polypeptide:c25] [gn:rpc25:ykl1:unf1] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggf:4.1:4.2] [sgdf:4.1.0:4.4.0.9.5.0] [db:gtc

CONTIG212	10975300_c3_18	3926	18029	462	154	YKL067W	571	1.8(10)-55	Saccharomyces cerevisiae	[ui:ykl067w] [pn:nucleoside diphosphate kinase:ndk:ndp kinase] [gn:ndk1:yнк1:yнк1333] [gtcf:4.1:4.2:12.13] [ec:2.7.4.6] [keggf:4.1:4.2] [sgdf:1.3.8:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2321	20709436_c3_9	3927	18030	516	172	YLR432W	585	6.0(10)-57	Saccharomyces cerevisiae	[ui:ylr432w] [pn:strong similarity to imp dehydrogenases, pur5p and yml056c:probable inosine-5"-monophosphate dehydrogenase:imp dehydrogenase:impdh:impd] [gn:i9753] [gtcf:4.1] [ec:1.1.1.205] [keggf:4.1] [sgdf:1.3.1] [db:gtc-sacchar
CONTIG2321	35189768_c2_7	3928	18031	195	65	YLR432W	238	2.2(10)-19	Saccharomyces cerevisiae	[ui:ylr432w] [pn:strong similarity to imp dehydrogenases, pur5p and yml056c:probable inosine-5"-monophosphate dehydrogenase:imp dehydrogenase:impdh:impd] [gn:i9753] [gtcf:4.1] [ec:1.1.1.205] [keggf:4.1] [sgdf:1.3.1] [db:gtc-sacchar
CONTIG2321	10553150_c2_6	3929	18032	348	116	YML056C	264	3.1(10)-22	Saccharomyces cerevisiae	[ui:yml056c] [pn:strong similarity to imp dehydrogenases:probable inosine-5"-monophosphate dehydrogenase:imp dehydrogenase:impdh:impd] [gn:ym9958] [gtcf:4.1] [ec:1.1.1.205] [keggf:4.1] [sgdf:1.3.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5734	21879412_f2_3	3930	18033	600	200	YML022W	616	3.2(10)-60	Saccharomyces cerevisiae	[ui:yml022w] [pn:adenine phosphoribosyltransferase:adenine [gn:apt1] [gtcf:4.1] [ec:2.4.2.7] [keggfc:4.1] [sgdfc:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2652	24220307_f2_3	3931	18034	252	84	YMR120C	342	1.3(10)-30	Saccharomyces cerevisiae	[ui:yml120c] [pn:strong similarity to chicken purh bifunctional enzyme:phosphoribosylaminoimida zolecarboxamide formyltransferase 2-aicar transformylase / imp cyclohydrolase:inosinica:imp synthetase:atic] [gn:adel7:ym8564] [gtcf:4.1]
CONTIG5413	5292599_c1_13	3932	18035	1314	438	YMR120C	1757	3.8(10)-181	Saccharomyces cerevisiae	[ui:yml120c] [pn:strong similarity to chicken purh bifunctional enzyme:phosphoribosylaminoimida zolecarboxamide formyltransferase 2-aicar transformylase / imp cyclohydrolase:inosinica:imp synthetase:atic] [gn:adel7:ym8564] [gtcf:4.1]
CONTIG3970	29961567_c3_13	3933	18036	633	211	YMR217W	860	4.4(10)-86	Saccharomyces cerevisiae	[ui:yml217w] [pn:glutamine-hydrolyzing:gmp synthase:glutamine-hydrolysing:glutamine amidotransferase:gmp synthetase] [gn:gual:ym8261] [gtcf:4.1:5.1] [ec:6.3.5.2] [keggfc:4.1:5.1] [sgdfc:1.3.1] [db:gtc-saccharomyces cerevisiae]

CONTIG3970	4725875_c1_10	3934	18037	987	329	YMR217W	1214	1.3(10)-123	Saccharomyces cerevisiae	[ui:ymr217w] [pn:glutamine-hydrolyzing:gmp synthase:glutamine amidotransferase:gmp synthetase] [gn:gua1:ym8261] [gtcf:4.1:5.1] [ec:3.5.2] [keggf:4.1:5.1] [sgdf:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4054	19534511_f3_2	3935	18038	1629	543	YMR300C	1726	7.2(10)-182	Saccharomyces cerevisiae	[ui:ymr300c] [pn:amidophosphoribosyltransferase:glutamine phosphoribosylpyrophosphate amidotransferase:atase] [gn:ade4:ym9952] [gtcf:4.1:5.1] [ec:2.4.2.14] [keggf:4.1:5.1] [sgdf:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1807	23945782_c1_1	3936	18039	576	192	YNL262W	179	2.0(10)-15	Saccharomyces cerevisiae	[ui:ynl262w] [pn:dna-directed dna polymerase epsilon, catalytic subunit a:dna polymerase epsilon, catalytic subunit a:dna polymerase ii subunit a] [gn:pol2:dun2:n0825] [gtcf:4.1:4.2:10.1:10.10:10.2:10.8:12.8] [ec:2.7.7] [keggf:4.1]
CONTIG3404	10198957_f2_1	3937	18040	1839	613	YNL262W	1408	3.5(10)-143	Saccharomyces cerevisiae	[ui:ynl262w] [pn:dna-directed dna polymerase epsilon, catalytic subunit a:dna polymerase epsilon, catalytic subunit a:dna polymerase ii subunit a] [gn:pol2:dun2:n0825] [gtcf:4.1:4.2:10.1:10.10:10.2:10.8:12.8] [ec:2.7.7] [keggf:4.1]

CONTIG650	255192_fl_1	3938	18041	699	233	YNL262W	1076	1.3(10)-107	Saccharomyces cerevisiae	[ui:ynl262w] [pn:dna-directed dna polymerase epsilon, catalytic subunit a:dna polymerase epsilon, catalytic subunit a:dna polymerase ii subunit a] [gn:pol2:dun2:n0825] [gfcf:4.1:4.2:10.1:10.10:10.2:10.8:12.8] [ec:2.7.7.7] [keggfc:4.1
CONTIG650	781538_fl_2	3939	18042	459	153	YNL262W	539	2.0(10)-50	Saccharomyces cerevisiae	[ui:ynl262w] [pn:dna-directed dna polymerase epsilon, catalytic subunit a:dna polymerase epsilon, catalytic subunit a:dna polymerase ii subunit a] [gn:pol2:dun2:n0825] [gfcf:4.1:4.2:10.1:10.10:10.2:10.8:12.8] [ec:2.7.7.7] [keggfc:4.1
b1x18543.y	21519057_c3_2	3940	18043	525	175	YNL262W	701	1.2(10)-67	Saccharomyces cerevisiae	[ui:ynl262w] [pn:dna-directed dna polymerase epsilon, catalytic subunit a:dna polymerase epsilon, catalytic subunit a:dna polymerase ii subunit a] [gn:pol2:dun2:n0825] [gfcf:4.1:4.2:10.1:10.10:10.2:10.8:12.8] [ec:2.7.7.7] [keggfc:4.1
b1x18984.y	19689090_c1_2	3941	18044	522	174	YNL262W	355	7.5(10)-31	Saccharomyces cerevisiae	[ui:ynl262w] [pn:dna-directed dna polymerase epsilon, catalytic subunit a:dna polymerase epsilon, catalytic subunit a:dna polymerase ii subunit a] [gn:pol2:dun2:n0825] [gfcf:4.1:4.2:10.1:10.10:10.2:10.8:12.8] [ec:2.7.7.7] [keggfc:4.1

CONTIG5289	3361885_c3_14	3942	18045	1197	399	YNL248C	1049	4.0(10)-106	Saccharomyces cerevisiae	[ui:ynl248c] [pn:dna-directed ma polymerase a.i chain, 46 kda:dna-directed rna polymerase i 49 kd polypeptide:a49] [gn:rpa49:rm13:n0880] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggf:4.1:4.2] [sgdf:4.1.0:9.5.0] [db:gtc-saccha
CONTIG5615	34064057_f2_9	3943	18046	1302	434	YNL220W	1553	1.6(10)-159	Saccharomyces cerevisiae	[ui:ynl220w] [pn:adenylosuccinate synthetase:imp--aspartate ligase] [gn:ade12:n1290] [gtcf:4.1:5.2:10.1:10.2] [ec:6.3.4.4] [keggf:4.1:5.2] [sgdf:1.3.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4968	21619037_c2_3	3944	18047	1074	358	YNL141W	1117	2.6(10)-113	Saccharomyces cerevisiae	[ui:ynl141w] [pn:similarity to adenosine deaminase:probable adenosine deaminase:adenosine aminohydrolase] [gn:n1208:n1825] [gtcf:4.1] [ec:3.5.4.4] [keggf:4.1] [sgdf:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4701	815686_c2_11	3945	18048	195	65	YNL113W	116	3.0(10)-7	Saccharomyces cerevisiae	[ui:ynl113w] [pn:dna-directed ma polymerase i,iii 16 kd subunit:dna-directed rna polymerases i and iii 16 kd polypeptide:ac19] [gn:rpc19:n1937] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggf:4.1:4.2] [sgdf:4.1.0:4.4.0:9.5.0] [d

CONTIG320	6835817_f2_1	3946	18049	711	237	YNL102W	626	5.0(10)-60	Saccharomyces cerevisiae	[ui:ynl102w] [pn:dna-directed dna polymerase alpha, 180 kd subunit:dna polymerase alpha:dna polymerase i] [gn:pol1:cdc17:n2181] [gicfc:4.1:4.2:10.1:10.2:10.8] [ec:2.7.7.7] [keggfc:4.1:4.2] [sgdfe:3.6.0:9.5.0] [db:gtc-saccharomyces cer
CONTIG3485	10962757_c2_4	3947	18050	417	139	YNL102W	216	2.7(10)-16	Saccharomyces cerevisiae	[ui:ynl102w] [pn:dna-directed dna polymerase alpha, 180 kd subunit:dna polymerase alpha:dna polymerase i] [gn:pol1:cdc17:n2181] [gicfc:4.1:4.2:10.1:10.2:10.8] [ec:2.7.7.7] [keggfc:4.1:4.2] [sgdfe:3.6.0:9.5.0] [db:gtc-saccharomyces cer
CONTIG4421	11737878_c2_2	3948	18051	1956	652	YNL102W	1983	4.4(10)-205	Saccharomyces cerevisiae	[ui:ynl102w] [pn:dna-directed dna polymerase alpha, 180 kd subunit:dna polymerase alpha:dna polymerase i] [gn:pol1:cdc17:n2181] [gicfc:4.1:4.2:10.1:10.2:10.8] [ec:2.7.7.7] [keggfc:4.1:4.2] [sgdfe:3.6.0:9.5.0] [db:gtc-saccharomyces cer

CONTIG921	5110343_f2_2	3949	18052	759	253	YNL102W	298	5.0(10)-25	Saccharomyces cerevisiae	[ui:ynl102w] [pn:dna-directed dna polymerase alpha, 180 kd subunit:dna polymerase alpha:dna polymerase i] [gn:pol1:cdc17:n2181] [gtcf:4.1:4.2:10.1:10.2:10.8] [ec:2.7.7.7] [keggf:4.1:4.2] [sgdf:3.6.0:9.5.0] [db:gtc-saccharomyces cer
b3x16086.y	6301575_c3_4	3950	18053	756	252	YNL102W	456	7.2(10)-42	Saccharomyces cerevisiae	[ui:ynl102w] [pn:dna-directed dna polymerase alpha, 180 kd subunit:dna polymerase alpha:dna polymerase i] [gn:pol1:cdc17:n2181] [gtcf:4.1:4.2:10.1:10.2:10.8] [ec:2.7.7.7] [keggf:4.1:4.2] [sgdf:3.6.0:9.5.0] [db:gtc-saccharomyces cer
CONTIG5595	85067_f2_3	3951	18054	1080	360	YNR003C	618	1.8(10)-60	Saccharomyces cerevisiae	[ui:ynr003c] [pn:dna-directed rna polymerase iii, 34 kd subunit:dna-directed rna polymerase iii 36 kd polypeptide:c34] [gn:rpc34:n2031] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggf:4.1:4.2] [sgdf:4.1.0:4.4.0:9.5.0] [db:gtc-sac
CONTIG4369	4881567_f2_5	3952	18055	324	108	YOL005C	316	1.8(10)-28	Saccharomyces cerevisiae	[ui:yol005c] [pn:dna-directed rna polymerase ii subunit, 13.6 kd:dna-directed rna polymerase ii 13.6 kd polypeptide:b13.6] [gn:rpb11] [gtcf:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggf:4.1:4.2] [sgdf:4.8.1:9.5.0] [db:gtc-saccharomyces ce

CONTIG3996	16663306_f3_5	3953	18056	531	177	YOR116C	653	6.5(10)-63	Saccharomyces cerevisiae	[ui:yor116c] [pn:dna-directed mna polymerase iii, 160 kd subunit:dna-directed mna polymerase iii largest subunit:c160] [gn:rpc1:rho31:rpc160:o3254:yor3254c] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:4.4]
CONTIG5508	4507817_c1_20	3954	18057	3771	1257	YOR116C	4914	0	Saccharomyces cerevisiae	[ui:yor116c] [pn:dna-directed mna polymerase iii, 160 kd subunit:dna-directed mna polymerase iii largest subunit:c160] [gn:rpc1:rho31:rpc160:o3254:yor3254c] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:4.4]
CONTIG3224	22158568_c1_5	3955	18058	1680	560	YOR128C	2004	2.6(10)-207	Saccharomyces cerevisiae	[ui:yor128c] [pn:phosphoribosylaminoimidazole carboxylase:air carboxylase:airc] [gn:ade2:o3293:yor3293c] [gtcf:4.1] [ec:4.1.1.21] [keggfc:4.1] [sgdfc:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2733	20585037_c3_4	3956	18059	1230	410	YOR151C	1658	1.2(10)-170	Saccharomyces cerevisiae	[ui:yor151c] [pn:dna-directed mna polymerase ii, 140 kda chain:dna-directed mna polymerase ii 140 kd polypeptide:b150:mna polymerase ii subunit 2] [gn:rbp2:rho22:rbp150] [gtcf:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:4.4]

CONTIG425	21564188_c3_4	3957	18060	993	331	YOR151C	1180	5.4(10)-120	Saccharomyces cerevisiae	[ui:yor151c] [pn:dna-directed ma polymerase ii, 140 kda chain:dna-directed ma polymerase ii 140 kd polypeptide:b150:ma polymerase ii subunit 2] [gn:rpb2:rpo22:rpb150] [gtcf:4.1:4.2:10.1:10.2] [ec:2.7.7.6] [keggf:4.1:4.2] [sgdfc:4
CONTIG5807	14500763_f2_3	3958	18061	198	66	YOR207C	137	5.2(10)-8	Saccharomyces cerevisiae	[ui:yor207c] [pn:dna-directed ma polymerase iii, 130 kd subunit:dna-directed ma polymerase iii 130 kd polypeptide:c128:ma polymerase iii subunit 2] [gn:rpc2:rpc128:ret1] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggf:4.1:4.2]
CONTIG5807	10738878_f3_8	3959	18062	3183	1061	YOR207C	4483	0	Saccharomyces cerevisiae	[ui:yor207c] [pn:dna-directed ma polymerase iii, 130 kd subunit:dna-directed ma polymerase iii 130 kd polypeptide:c128:ma polymerase iii subunit 2] [gn:rpc2:rpc128:ret1] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggf:4.1:4.2]
CONTIG1069	2751432_f2_1	3960	18063	375	125	YOR224C	322	4.5(10)-29	Saccharomyces cerevisiae	[ui:yor224c] [pn:dna-directed ma polymerase i, ii, iii 16 kd subunit:dna-directed ma polymerases i, ii, and iii 14.5 kd polypeptide:abc14.4] [gn:rpb8:yor50-14] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggf:4.1:4.2] [sgdfc:4.1.

CONTIG5560	24251575_c3_21	3961	18064	942	314	YOR340C	400	3.7(10)-52	Saccharomyces cerevisiae	[ui:yor340c] [pn:dna-directed ma polymerase i, 36 kd subunit:dna-dependent ma polymerase 36 kd polypeptide:a43] [gn:rp43:rm12:o6271] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:9.5.0] [db:gtc-saccharo
CONTIG4460	6344192_f1_1	3962	18065	1389	463	YOR341W	1367	8.0(10)-144	Saccharomyces cerevisiae	[ui:yor341w] [pn:dna-directed ma polymerase i, 190 kd alpha subunit:dna-directed ma polymerase i 190 kd polypeptide:a190] [gn:rp41:rp4190:rm1:o6276] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:9.5.0] [
CONTIG4563	15126942_f2_1	3963	18066	2337	779	YOR341W	2455	4.2(10)-255	Saccharomyces cerevisiae	[ui:yor341w] [pn:dna-directed ma polymerase i, 190 kd alpha subunit:dna-directed ma polymerase i 190 kd polypeptide:a190] [gn:rp41:rp4190:rm1:o6276] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:9.5.0] [

CONTIG4776	33854637_c2_7	3964	18067	477	159	YOR341W	583	2.6(10)-55	Saccharomyces cerevisiae	[ui:yor341w] [pn:dna-directed ma polymerase i, 190 kd alpha subunit:dna-directed ma polymerase i 190 kd polypeptide:a190] [gn:rpai:rpai90:rrm1:o6276] [gtcf:4.1.4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1.4.2] [sgdfc:4.1.0.9.5.0] [
CONTIG4468	25587567_f3_4	3965	18068	963	321	YOR360C	325	3.0(10)-37	Saccharomyces cerevisiae	[ui:yor360c] [pn:high affinity 3",5"-cyclic-nucleotide phosphodiesterase:3",5"-cyclic-nucleotide phosphodiesterase 2:pdease 2:high-affinity camp phosphodiesterase] [gn:pde2:sra5] [gtcf:4.1] [ec:3.1.4.17] [keggfc:4.1] [sgdfc:1.3.4.9.2
CONTIG1317	14652037_f2_2	3966	18069	825	275	YPL167C	304	1.2(10)-25	Saccharomyces cerevisiae	[ui:ypl167c] [pn:dna-directed dna polymerase zeta:probable dna polymerase] [gn:rev3:psol:p2535] [gtcf:4.1.4.2:10.1:10.10.2:10.8] [ec:2.7.7.7] [keggfc:4.1.4.2] [sgdfc:3.6.0.3.7.0.9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3778	11047833_f3_4	3967	18070	1380	460	YPL167C	1047	1.7(10)-105	Saccharomyces cerevisiae	[ui:ypl167c] [pn:dna-directed dna polymerase zeta:probable dna polymerase] [gn:rev3:psol:p2535] [gtcf:4.1.4.2:10.1:10.10.2:10.8] [ec:2.7.7.7] [keggfc:4.1.4.2] [sgdfc:3.6.0.3.7.0.9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG4564	11893778_f1_1	3968	18071	2013	671	YPR010C	2859	6.5(10)-298	Saccharomyces cerevisiae	[ui:ypr010c] [pn:dna-directed rna polymerase i, 135 kd subunit:dna-directed rna polymerase i 135 kd polypeptide:a135:ma polymerase i subunit 2] [gn:rapa2:rapa135:srp3:rm2:yp9531] [gtcfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1]
CONTIG4759	35830216_c3_15	3969	18072	1029	343	YPR010C	1479	1.1(10)-151	Saccharomyces cerevisiae	[ui:ypr010c] [pn:dna-directed rna polymerase i, 135 kd subunit:dna-directed rna polymerase i 135 kd polypeptide:a135:ma polymerase i subunit 2] [gn:rapa2:rapa135:srp3:rm2:yp9531] [gtcfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1]
CONTIG2746	26854067_f2_3	3970	18073	291	97	YPR110C	379	4.0(10)-35	Saccharomyces cerevisiae	[ui:ypr110c] [pn:dna-directed rna polymerase i, iii 40 kd subunit:dna-directed rna polymerases i and iii 40 kd polypeptide:ac40] [gn:rpe5:rpe40:p8283] [gtcfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:4.4.0:9.5]
b2x18990.y	29332812_c3_2	3971	18074	780	260	YPR110C	772	9.3(10)-77	Saccharomyces cerevisiae	[ui:ypr110c] [pn:dna-directed rna polymerase i, iii 40 kd subunit:dna-directed rna polymerases i and iii 40 kd polypeptide:ac40] [gn:rpe5:rpe40:p8283] [gtcfc:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggfc:4.1:4.2] [sgdfc:4.1.0:4.4.0:9.5]

CONTIG5261	16226437_fl_2	3972	18075	2196	732	YPR175W	613	3.1(10)-112	Saccharomyces cerevisiae	[ui:ypr175w] [pn:dna-directed dna polymerase epsilon, subunit b:dna polymerase epsilon, subunit b:dna polymerase ii subunit b] [gn:dpb2:p9705] [gtcf:4.1:4.2:10.1:10.2:10.8] [ec:2.7.7.7] [keggf:4.1:4.2] [sgdfc:3.6.0:9.5.0] [db:gtc-sa]
b3x16016.y	24120192_fl_1	3973	18076	744	248	YPR175W	170	8.0(10)-12	Saccharomyces cerevisiae	[ui:ypr175w] [pn:dna-directed dna polymerase epsilon, subunit b:dna polymerase epsilon, subunit b:dna polymerase ii subunit b] [gn:dpb2:p9705] [gtcf:4.1:4.2:10.1:10.2:10.8] [ec:2.7.7.7] [keggf:4.1:4.2] [sgdfc:3.6.0:9.5.0] [db:gtc-sa]
CONTIG3838	23992000_c3_5	3974	18077	414	138	YPR187W	375	1.1(10)-34	Saccharomyces cerevisiae	[ui:ypr187w] [pn:dna-directed rna polymerase i, ii, iii 18 kd subunit:dna-directed rna polymerases i, ii, and iii 23 kd polypeptide:abc23] [gn:rpb6:rpo26:p9677] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggf:4.1:4.2] [sgdfc:4.1.0]
CONTIG2927	11933333_c2_3	3975	18078	435	145	YPR190C	190	5.2(10)-14	Saccharomyces cerevisiae	[ui:ypr190c] [pn:dna-directed rna polymerase iii, 82 kd subunit:dna-directed rna polymerase iii 74 kd polypeptide:c74] [gn:rpc3:rpc82] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggf:4.1:4.2] [sgdfc:4.1.0:4.4.0:9.5.0] [db:gtc-sacc]

b3x16424.x	26256451_f3_1	3976	18079	501	167	YPR190C	217	6.5(10)-17	Saccharomyces cerevisiae	[ui:ypr190c] [pn:dna-directed ma polymerase iii, 82 kd subunit:dna-directed ma polymerase iii 74 kd polypeptide:c74] [gn:rpc3:rpc82] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggf:4.1:4.2] [sgdfc:4.1.0:4.4.0:9.5.0] [db:gtc-sacc
b3x10245.x	36613775_f3_1	3977	18080	528	176	YPR190C	170	7.2(10)-12	Saccharomyces cerevisiae	[ui:ypr190c] [pn:dna-directed ma polymerase iii, 82 kd subunit:dna-directed ma polymerase iii 74 kd polypeptide:c74] [gn:rpc3:rpc82] [gtcf:4.1:4.2:10.1:10.2:10.3] [ec:2.7.7.6] [keggf:4.1:4.2] [sgdfc:4.1.0:4.4.0:9.5.0] [db:gtc-sacc
CONTIG5421	10722537_f1_3	3978	18081	807	269	YDR020C	227	5.2(10)-19	Saccharomyces cerevisiae	[ui:ydr020c] [pn:weak similarity to uridine kinases and phosphoribulokinases] [gtcf:4.1] [keggf:14.2] [sgdfc:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4793	34063317_c3_12	3979	18082	738	246	YLR017W	598	2.5(10)-58	Saccharomyces cerevisiae	[ui:ylr017w] [pn:multiple enhancer of uas2] [gtcf:4.1] [keggf:14.2] [sgdfc:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5059	11719632_c2_12	3980	18083	600	200	YLR209C	573	1.1(10)-55	Saccharomyces cerevisiae	[ui:ylr209c] [pn:strong similarity to purine-nucleoside phosphorylases] [gtcf:4.1] [keggf:14.2] [sgdfc:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4096	13173265_f1_1	3981	18084	1200	400	YLR359W	1657	1.5(10)-170	Saccharomyces cerevisiae	[ui:ylr359w] [pn:strong similarity to adenylosuccinate lyase] [gtcf:4.1] [keggf:14.2] [sgdfc:1.3.1] [db:gtc-saccharomyces cerevisiae]

CONTIG4096	5191511_f2_2	3982	18085	297	99	YLR359W	344	2.1(10)-31	Saccharomyces cerevisiae	[ui:ylr359w] [pn:strong similarity to adenylosuccinate lyase] [gtcf:4.1] [keggf:14.2] [sgdf:1.3.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5658	24413962_f3_10	3983	18086	1419	473	YOL061W	746	7.7(10)-118	Saccharomyces cerevisiae	[ui:yol061w] [pn:similarity to ribose-phosphate pyrophosphokinases] [gtcf:4.1:4.2] [keggf:14.2] [sgdf:1.3.1:1.3.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1898	25600913_c3_6	3984	18087	636	212	YOR280C	223	1.3(10)-18	Saccharomyces cerevisiae	[ui:yor280c] [pn:similarity to s.pombe dihydrofolate reductase] [gtcf:10.7:9.6] [keggf:14.2] [sgdf:1.1:1.3.1:1.3.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5650	9773432_c2_20	3985	18088	822	274	YOR280C	199	4.9(10)-16	Saccharomyces cerevisiae	[ui:yor280c] [pn:similarity to s.pombe dihydrofolate reductase] [gtcf:10.7:9.6] [keggf:14.2] [sgdf:1.1:1.3.1:1.3.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2843	24228192_c1_4	3986	18089	1200	400	YOL081W	478	9.6(10)-44	Saccharomyces cerevisiae	[ui:yol081w] [pn:gtpase-activating protein for ras proteins:inhibitory regulator protein ira2] [gn:ira2:glc4:ccs1:o0985] [gtcf:4.1:10.2:11.1] [keggf:14.2] [sgdf:1.3.4:1.3.5:9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4914	35369027_c3_10	3987	18090	2235	745	YOL081W	468	4.7(10)-41	Saccharomyces cerevisiae	[ui:yol081w] [pn:gpase-activating protein for ras proteins:inhibitory regulator protein ira2] [gn:ira2:glc4:ccs1:o0985] [gtcf:4.1:10.2:11.1] [keggf:14.2] [sgdfc:1.3.4:1.3.5.9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5564	4696963_t2_5	3988	18091	3849	1283	YOL081W	287	3.0(10)-25	Saccharomyces cerevisiae	[ui:yol081w] [pn:gpase-activating protein for ras proteins:inhibitory regulator protein ira2] [gn:ira2:glc4:ccs1:o0985] [gtcf:4.1:10.2:11.1] [keggf:14.2] [sgdfc:1.3.4:1.3.5.9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3161	33204375_c1_2	3989	18092	1236	412	YPL212C	960	1.1(10)-96	Saccharomyces cerevisiae	[ui:ypl212c] [pn:pseudouridine synthase 1] [gn:pus1] [gtcf:4.1:10.1:10.2:10.6] [keggf:14.2] [sgdfc:1.3.4:4.6.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5516	563187_c3_22	3990	18093	519	173	YDL125C	412	1.3(10)-38	Saccharomyces cerevisiae	[ui:ydl125c] [pn:similarity to protein kinase c inhibitor-i] [gn:hnt1] [gtcf:4.1:12.13] [keggf:14.2] [sgdfc:1.3.8] [db:gtc-saccharomyces cerevisiae]

CONTIG5744	9817542_f3_12	3991	18094	654	218	YDR305C	374	1.3(10)-34	Saccharomyces cerevisiae	[ui:ydr305c] [pn:similarity to s.pombe diadenosine 5", 5" ^{nm} -p1.p4-tetraphosphate asymmetrical hydrolase:hypothetical 24.8 kd hit-like protein] [gn:hnt2.d9740] [gtcf:4.1.12.13] [keggf:14.2] [sgdf:1.3.8] [db:gtc-saccharomyces cerevisi]
CONTIG5324	4334811_f1_1	3992	18095	981	327	YBL039C	1161	5.5(10)-118	Saccharomyces cerevisiae	[ui:ybl039c] [pn:ctp synthase 1:uip-ammonia ligase 1:ctp synthetase 1] [gn:ura7:ybl0410] [gtcf:4.2] [ec:6.3.4.2] [keggf:4.2] [sgdf:1.3.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5324	20095662_f3_7	3993	18096	822	274	YBL039C	865	1.3(10)-86	Saccharomyces cerevisiae	[ui:ybl039c] [pn:ctp synthase 1:uip-ammonia ligase 1:ctp synthetase 1] [gn:ura7:ybl0410] [gtcf:4.2] [ec:6.3.4.2] [keggf:4.2] [sgdf:1.3.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1971	26366561_c2_7	3994	18097	267	89	YEL021W	256	4.4(10)-22	Saccharomyces cerevisiae	[ui:yel021w] [pn:orotidine-5"-phosphate decarboxylase:orotidine 5"-phosphate decarboxylase:omp decarboxylase] [gn:ura3] [gtcf:4.2] [ec:4.1.1.23] [keggf:4.2] [sgdf:1.3.2] [db:gtc-saccharomyces cerevisiae]

CONTIG698	25681512_f3_1	3995	18098	243	81	YEL021W	267	3.0(10)-23	Saccharomyces cerevisiae	[ui:yel021w] [pn:orotidine-5"-phosphate decarboxylase:orotidine 5"-phosphate decarboxylase:omp decarboxylase] [gn:ura3] [gtcf:4.2] [ec:4.1.1.23] [keggfc:4.2] [sgdfe:1.3.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5721	15672577_f2_9	3996	18099	657	219	YHR128W	833	3.2(10)-83	Saccharomyces cerevisiae	[ui:yhr128w] [pn:uracil phosphoribosyltransferase:ump pyrophosphorylase:uprtase] [gn:fur1] [gtcf:4.2] [ec:2.4.2.9] [keggfc:4.2] [sgdfe:1.3.2.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5552	26370762_c2_14	3997	18100	1074	358	YHR144C	701	3.1(10)-69	Saccharomyces cerevisiae	[ui:yhr144c] [pn:deoxycytidylate deaminase:dcmp deaminase] [gn:ded1] [gtcf:4.2] [ec:3.5.4.12] [keggfc:4.2] [sgdfe:1.3.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3304	402082_f2_1	3998	18101	1587	529	YJL130C	1122	1.6(10)-112	Saccharomyces cerevisiae	[ui:yjl130c] [pn:multifunctional pyrimidine biosynthesis protein:ura2 protein:contains:glutamine-dependent carbamoyl- phosphate synthase , aspartate carbamoyltransferase] [gn:ura2:j0686] [gtcf:4.2.5.1:5.2:10.1:10.2] [keggfc:4.2:5.1:5]

CONTIG3364	550776_c3_5	3999	18102	1026	342	YJL130C	1199	9.1(10)-121	Saccharomyces cerevisiae	[ui:yjl130c] [pn:multifunctional pyrimidine biosynthesis protein:ura2 protein:contains:glutamine-dependent carbamoyl- phosphate synthase , aspartate carbamoyltransferase] [gn:ura2:j0686] [gtcf:4.2.5.1:5.2:10.1:10.2] [keggfc:4.2.5.1:5
CONTIG4851	24620282_f3_7	4000	18103	4215	1405	YJL130C	5189	0	Saccharomyces cerevisiae	[ui:yjl130c] [pn:multifunctional pyrimidine biosynthesis protein:ura2 protein:contains:glutamine-dependent carbamoyl- phosphate synthase , aspartate carbamoyltransferase] [gn:ura2:j0686] [gtcf:4.2.5.1:5.2:10.1:10.2] [keggfc:4.2.5.1:5
CONTIG4854	24031654_c2_5	4001	18104	183	61	YJL130C	249	1.3(10)-19	Saccharomyces cerevisiae	[ui:yjl130c] [pn:multifunctional pyrimidine biosynthesis protein:ura2 protein:contains:glutamine-dependent carbamoyl- phosphate synthase , aspartate carbamoyltransferase] [gn:ura2:j0686] [gtcf:4.2.5.1:5.2:10.1:10.2] [keggfc:4.2.5.1:5

CONTIG5482	29303127_f1_4	4002	18105	756	252	YJR057W	471	7.2(10)-45	Saccharomyces cerevisiae	[ui:yjr057w] [pn:thymidylate kinase:dmp kinase] [gn:cdc8:j1715] [gtcf:4.2] [ec:2.7.4.9] [keggfc:4.2] [sgdfe:1.3.2.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4597	14551501_f2_4	4003	18106	1098	366	YLR420W	1186	1.3(10)-120	Saccharomyces cerevisiae	[ui:ylr420w] [pn:dihydroorotase:dhoase] [gn:ura4:19931] [gtcf:4.2] [ec:3.5.2.3] [keggfc:4.2] [sgdfe:1.3.2] [db:gtc-saccharomyces cerevisiae]
b9x10d12.y	20100776_f2_1	4004	18107	636	212	YML106W	538	5.7(10)-52	Saccharomyces cerevisiae	[ui:yml106w] [pn:orotate phosphoribosyltransferase:orotate phosphoribosyltransferase 1:opt] [gn:ura5:pyr5:ym8339] [gtcf:4.2] [ec:2.4.2.10] [keggfc:4.2] [sgdfe:1.3.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5672	21953277_f2_7	4005	18108	1734	578	YNR012W	1128	1.8(10)-114	Saccharomyces cerevisiae	[ui:ynr012w] [pn:uridine kinase:uridine monophosphokinase] [gn:urk1:n2050] [gtcf:4.2] [ec:2.7.1.48] [keggfc:4.2] [sgdfe:1.3.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2626	4297525_f3_2	4006	18109	870	290	YOR074C	768	5.0(10)-87	Saccharomyces cerevisiae	[ui:yor074c] [pn:thymidylate synthase:ts] [gn:tmp1:cdc21] [gtcf:4.2.9.6.10.1:10.2] [ec:2.1.1.45] [keggfc:4.2.9.7.9.8] [sgdfe:1.3.3.9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2698	21675305_f3_2	4007	18110	1044	348	YDL244W	1391	2.3(10)-142	Saccharomyces cerevisiae	[ui:ydl244w] [pn:strong similarity to thi5p, yjr156c, ynl332w and a.parasiticus, s.pombe nmt1 protein] [gtcf:4.2] [keggf:14.2] [sgdfc:1.3.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4457	24276687_c2_8	4008	18111	198	66	YKL024C	142	5.2(10)-10	Saccharomyces cerevisiae	[ui:ykl024c] [pn:uridine-monophosphate kinase:uridylylate kinase:uk:uridine monophosphate kinase:ump kinase] [gn:ura6:soc8] [gtcf:4.2:10.1:10.2:14.1] [ec:2.7.4.-] [keggf:14.1] [sgdfc:1.3.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5694	9775308_c2_22	4009	18112	558	186	YKL024C	350	4.9(10)-32	Saccharomyces cerevisiae	[ui:ykl024c] [pn:uridine-monophosphate kinase:uridylylate kinase:uk:uridine monophosphate kinase:ump kinase] [gn:ura6:soc8] [gtcf:4.2:10.1:10.2:14.1] [ec:2.7.4.-] [keggf:14.1] [sgdfc:1.3.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4935	29922786_c3_7	4010	18113	414	138	YPR062W	379	4.0(10)-35	Saccharomyces cerevisiae	[ui:ypr062w] [pn:cytosine deaminase] [gn:fcy1] [gtcf:4.2] [keggf:14.2] [sgdfc:1.3.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3827	1988817_fl_1	4011	18114	183	61	YDR513W	174	2.2(10)-13	Saccharomyces cerevisiae	[ui:ydr513w] [pn:glutaredoxin:thioltransferase] [gn:trt1:trt:d9719] [gtcf:4.2:12.12] [keggf:14.2] [sgdfc:1.3.3:9.2.0:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3812	4407680_f2_3	4012	18115	582	194	YDR513W	250	1.8(10)-21	Saccharomyces cerevisiae	[ui:ydr513w] [pn:glutaredoxin:thioltransferase] [gn:tr1:tr:d9719] [gtcf:4.2:12.12] [keggf:14.2] [sgdf:1.3:9.2.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5781	4541257_f1_2	4013	18116	1485	495	YOR269W	363	2.0(10)-33	Saccharomyces cerevisiae	[ui:yor269w] [pn:similarity to human lis-1 protein:protein] [gn:pac1] [gtcf:4.2] [keggf:14.2] [sgdf:1.3.3] [db:gtc-saccharomyces cerevisiae]
CONTIG1871	394062_c2_3	4014	18117	591	197	YPL059W	424	7.0(10)-40	Saccharomyces cerevisiae	[ui:ypl059w] [pn:similarity to glutaredoxins] [gtcf:4.2] [keggf:14.2] [sgdf:1.3.3] [db:gtc-saccharomyces cerevisiae]
b3x15471.y	35806566_f1_1	4015	18118	462	154	YJR062C	96	5.0(10)-10	Saccharomyces cerevisiae	[ui:yjr062c] [pn:amino-terminal amidase:n-terminal amidase] [gn:nta1:j1742] [gtcf:4.3:7.1:10.11:10.7] [ec:3.2.1.-] [keggf:4.3:4.4] [sgdf:6.3.0:6.5.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5489	24803187_f2_1	4016	18119	3015	1005	YGL173C	1767	3.3(10)-182	Saccharomyces cerevisiae	[ui:ygl173c] [pn:multifunctional nuclease:strand exchange protein 1:kar:- enhancing mutation protein:5"-3" exoribonuclease:dna strand transfer protein beta:stp-beta] [gn:kem1:sep1:xm1:dst2:rar5:g1645] [gtcf:4.4:10.10:10.3:12.8] [keg

CONTIG5671	4881511_f2_8	4017	18120	1206	402	YGL173C	1332	4.2(10)-136	Saccharomyces cerevisiae	[ui:ygl173c] [pn:multifunctional nuclease:strand exchange protein:5"-3" exoribonuclease:dna l:kar:- enhancing mutation strand transfer protein beta:stp-beta] [gn:kem1:sep1:xml:dst2:rar5:g1645] [gtcf:4.4:10:10:10:3:12.8] [keg
CONTIG2986	994087_f3_3	4018	18121	378	126	YGR195W	328	1.0(10)-29	Saccharomyces cerevisiae	[ui:ygr195w] [pn:weak similarity to p.aeruginosa mase ph:hypothetical 27.6 kd protein in pdx1-sng1 intergenic region] [gn:g7587] [gtcf:4.4:10:10] [keggf:14.2] [sgdfc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG1992	3580777_f1_1	4019	18122	1203	401	YHR077C	516	1.5(10)-48	Saccharomyces cerevisiae	[ui:yhr077c] [pn:nonsense-mediated mma decay protein 2:up- frameshift suppressor 2] [gn:nmd2:upf2:ifs1:sua1] [gtcf:4.4:10:10:10:7] [keggf:14.2] [sgdfc:1.3.6:5.3:0:9:2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3143	23634465_c1_5	4020	18123	879	293	YHR077C	108	6.4(10)-10	Saccharomyces cerevisiae	[ui:yhr077c] [pn:nonsense-mediated mma decay protein 2:up- frameshift suppressor 2] [gn:nmd2:upf2:ifs1:sua1] [gtcf:4.4:10:10:10:7] [keggf:14.2] [sgdfc:1.3.6:5.3:0:9:2.0] [db:gtc-saccharomyces cerevisiae]

b1x11358.y	915627_c2_4	4021	18124	756	252	YHR077C	92	0.32	Saccharomyces cerevisiae	[ui:yhr077c] [pn:nonsense-mediated mma decay protein 2:up- frameshift suppressor 2] [gn:nmd2:upf2:ifs1:sua1] [gtcf:4.4:10.10.7] [keggfc:14.2] [sgdfc:1.3.6:5.3.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2001	235451_c2_2	4022	18125	909	303	YJR132W	289	2.7(10)-24	Saccharomyces cerevisiae	[ui:yjr132w] [pn:nam7p/upflp-interacting protein:nonsense-mediated mma decay protein 5] [gn:nmd5:j2112] [gtcf:4.4:10.10] [keggfc:14.2] [sgdfc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG4962	9776538_fl_1	4023	18126	1212	404	YJR132W	344	3.7(10)-30	Saccharomyces cerevisiae	[ui:yjr132w] [pn:nam7p/upflp-interacting protein:nonsense-mediated mma decay protein 5] [gn:nmd5:j2112] [gtcf:4.4:10.10] [keggfc:14.2] [sgdfc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG4998	36371075_c2_13	4024	18127	1623	541	YJR132W	848	8.1(10)-85	Saccharomyces cerevisiae	[ui:yjr132w] [pn:nam7p/upflp-interacting protein:nonsense-mediated mma decay protein 5] [gn:nmd5:j2112] [gtcf:4.4:10.10] [keggfc:14.2] [sgdfc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG4998	4335001_c3_15	4025	18128	522	174	YJR132W	200	8.9(10)-15	Saccharomyces cerevisiae	[ui:yjr132w] [pn:nam7p/upflp-interacting protein:nonsense-mediated mma decay protein 5] [gn:nmd5:j2112] [gtcf:4.4:10.10] [keggfc:14.2] [sgdfc:1.3.6] [db:gtc-saccharomyces cerevisiae]

CONTIG5085	23650312_c1_8	4026	18129	1335	445	YJR132W	546	7.5(10)-52	Saccharomyces cerevisiae	[ui:yjr132w] [pn:nam7p/upflp-interacting protein:nonsense-mediated mrna decay protein 5] [gn:nmd5;j2112] [gtcf:4.4:10.10] [keggf:14.2] [sgdfc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG5757	4879063_f3_5	4027	18130	1458	486	YKL149C	597	1.8(10)-64	Saccharomyces cerevisiae	[ui:ykl149c] [pn:lariat-debranching enzyme:lariat debranching enzyme] [gn:dbp1:prp26:ykl604] [gtcf:4.4:10.1:10.10:10.2:14.1] [ec:3.1.-.-] [keggf:14.1] [sgdfc:1.3.6:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5776	14241436_f2_12	4028	18131	1242	414	YLR363C	139	9.6(10)-15	Saccharomyces cerevisiae	[ui:yrl363c] [pn:nam7p/upflp-interacting protein] [gn:nmd4] [gtcf:4.4:10.10] [keggf:14.2] [sgdfc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG5769	23612501_c3_20	4029	18132	1155	385	YMR080C	1115	4.2(10)-113	Saccharomyces cerevisiae	[ui:ymr080c] [pn:nonsense-mediated mrna decay protein:nam7 protein:nonsense-mediated mrna decay protein 1:up-frameshift suppressor 1] [gn:nam7:upfl:ifs2:mof4:ym9582] [gtcf:4.4:10.10:10.7] [keggf:14.2] [sgdfc:1.3.6:5.3.0:9.2.0] [db:g

CONTIG628	35937828_f3_1	4030	18133	537	179	YMR080C	196	2.1(10)-14	Saccharomyces cerevisiae	[ui:ymr080c] [pn:nonsense-mediated mma decay protein:nam7 protein:nonsense-mediated mma decay protein 1:up-frameshift suppressor 1] [gn:nam7:upf1:ifs2:mof4:ym9582] [gtcf:4.4:10:10.7] [keggf:14.2] [sgdf:1.3.6:5.3.0:9.2.0] [db:g
CONTIG819	15838508_c3_2	4031	18134	321	107	YMR080C	355	2.1(10)-31	Saccharomyces cerevisiae	[ui:ymr080c] [pn:nonsense-mediated mma decay protein:nam7 protein:nonsense-mediated mma decay protein 1:up-frameshift suppressor 1] [gn:nam7:upf1:ifs2:mof4:ym9582] [gtcf:4.4:10:10.7] [keggf:14.2] [sgdf:1.3.6:5.3.0:9.2.0] [db:g
CONTIG819	5985882_c3_1	4032	18135	594	198	YMR080C	744	8.5(10)-74	Saccharomyces cerevisiae	[ui:ymr080c] [pn:nonsense-mediated mma decay protein:nam7 protein:nonsense-mediated mma decay protein 1:up-frameshift suppressor 1] [gn:nam7:upf1:ifs2:mof4:ym9582] [gtcf:4.4:10:10.7] [keggf:14.2] [sgdf:1.3.6:5.3.0:9.2.0] [db:g
CONTIG3369	15078550_c1_5	4033	18136	288	96	YMR234W	116	4.2(10)-11	Saccharomyces cerevisiae	[ui:ymr234w] [pn:ribonuclease h:mase h] [gn:mh1:ym9959] [gtcf:4.4:10.10] [ec:3.1.26.4] [keggf:14.1] [sgdf:1.3.6] [db:gtc-saccharomyces cerevisiae]

CONTIG3369	4103127_c2_6	4034	18137	723	241	YMR234W	151	1.8(10)-17	Saccharomyces cerevisiae	[ui:yvr234w] [pn:ribonuclease h:mase h] [gn:rmh1:ym9959] [gtcf:4.4:10.10] [ec:3.1.26.4] [keggf:14.1] [sgdfc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG5034	581250_f3_8	4035	18138	960	320	YMR234W	217	6.0(10)-31	Saccharomyces cerevisiae	[ui:yvr234w] [pn:ribonuclease h:mase h] [gn:rmh1:ym9959] [gtcf:4.4:10.10] [ec:3.1.26.4] [keggf:14.1] [sgdfc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG1638	33478461_c3_3	4036	18139	759	253	YOR033C	329	6.2(10)-29	Saccharomyces cerevisiae	[ui:yvr033c] [pn:exo1 encodes an exonuclease which interacts with msh2p:dhs1 protein] [gn:dhs1:or26] [gtcf:4.4:10.10:10.8] [keggf:14.2] [sgdfc:1.3.6:3.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3402	1375_fl_1	4037	18140	822	274	YPL123C	491	5.5(10)-47	Saccharomyces cerevisiae	[ui:ypl123c] [pn:similarity to ribonucleases] [gtcf:4.4:10.10] [keggf:14.2] [sgdfc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG4791	35158411_c3_8	4038	18141	1047	349	YPL123C	546	8.3(10)-53	Saccharomyces cerevisiae	[ui:ypl123c] [pn:similarity to ribonucleases] [gtcf:4.4:10.10] [keggf:14.2] [sgdfc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG4791	4490937_c2_6	4039	18142	291	97	YPL123C	92	0.00097	Saccharomyces cerevisiae	[ui:ypl123c] [pn:similarity to ribonucleases] [gtcf:4.4:10.10] [keggf:14.2] [sgdfc:1.3.6] [db:gtc-saccharomyces cerevisiae]
CONTIG5758	20119703_c3_24	4040	18143	999	333	YPL123C	430	1.6(10)-40	Saccharomyces cerevisiae	[ui:ypl123c] [pn:similarity to ribonucleases] [gtcf:4.4:10.10] [keggf:14.2] [sgdfc:1.3.6] [db:gtc-saccharomyces cerevisiae]

CONTIG117	13867916_f3_1	4041	18144	660	220	YGL245W	931	1.3(10)-93	Saccharomyces cerevisiae	[ui:ygl245w] [pn:strong similarity to glutamine--trna ligase:glutamyl-trna synthetase, cytoplasmic:glutamate-- trna ligase:glurs:p85] [gn:g0583:hrb724] [gtcf:5.1.9.10:10.6] [ec:6.1.1.17] [keggfc:5.1.9.10:10.1:10.2] [sgdfe:5.4.0] [db:
CONTIG1607	4507691_fl_1	4042	18145	633	211	YGL245W	648	1.3(10)-63	Saccharomyces cerevisiae	[ui:ygl245w] [pn:strong similarity to glutamine--trna ligase:glutamyl-trna synthetase, cytoplasmic:glutamate-- trna ligase:glurs:p85] [gn:g0583:hrb724] [gtcf:5.1.9.10:10.6] [ec:6.1.1.17] [keggfc:5.1.9.10:10.1:10.2] [sgdfe:5.4.0] [db:
CONTIG2711	9876292_c2_4	4043	18146	666	222	YGL245W	288	1.8(10)-24	Saccharomyces cerevisiae	[ui:ygl245w] [pn:strong similarity to glutamine--trna ligase:glutamyl-trna synthetase, cytoplasmic:glutamate-- trna ligase:glurs:p85] [gn:g0583:hrb724] [gtcf:5.1.9.10:10.6] [ec:6.1.1.17] [keggfc:5.1.9.10:10.1:10.2] [sgdfe:5.4.0] [db:
CONTIG3361	4969505_f2_1	4044	18147	894	298	YJL101C	493	3.3(10)-47	Saccharomyces cerevisiae	[ui:yjl101c] [pn:glutamate--cysteine ligase:gamma-glutamylcysteine synthetase:gamma-ecs:gcs] [gn:gsh1:j0832] [gtcf:5.1.6.16:12.12] [ec:6.3.2.2] [keggfc:5.1:6.9] [sgdfe:11.3.0] [db:gic-saccharomyces cerevisiae]

CONTIG3361	23944202_f3_2	4045	18148	609	203	YJL101C	200	4.5(10)-15	Saccharomyces cerevisiae	[ui:yjl101c] [pn:glutamate--cysteine ligase:gamma-glutamylcysteine synthetase:gamma-ecs:gs] [gn:gsh1:j0832] [gtcf:5.1:6.16:12.12] [ec:6.3.2.2] [keggfc:5.1:6.9] [sgdfe:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG780	34570275_c3_1	4046	18149	528	176	YJL101C	374	7.0(10)-34	Saccharomyces cerevisiae	[ui:yjl101c] [pn:glutamate--cysteine ligase:gamma-glutamylcysteine synthetase:gamma-ecs:gs] [gn:gsh1:j0832] [gtcf:5.1:6.16:12.12] [ec:6.3.2.2] [keggfc:5.1:6.9] [sgdfe:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1307	25634793_c3_2	4047	18150	498	166	YJR109C	443	1.1(10)-40	Saccharomyces cerevisiae	[ui:yjr109c] [pn:arginine-specific carbamoylphosphate synthase, large chain:carbamoyl-phosphate synthase, arginine-specific, large chain:arginine-specific carbamoyl-phosphate synthetase, ammonia chain] [gn:cpa2:j2002] [gtcf:5.1:6.6]
CONTIG4268	47250_f2_4	4048	18151	1263	421	YJR109C	1449	1.7(10)-148	Saccharomyces cerevisiae	[ui:yjr109c] [pn:arginine-specific carbamoylphosphate synthase, large chain:carbamoyl-phosphate synthase, arginine-specific, large chain:arginine-specific carbamoyl-phosphate synthetase, ammonia chain] [gn:cpa2:j2002] [gtcf:5.1:6.6]

CONTIG4268	7032513_f3_5	4049	18152	915	305	YJR109C	1108	2.2(10)-112	Saccharomyces cerevisiae	[ui:yjr109c] [pn:arginine-specific carbamoylphosphate synthase, large chain:carbamoyl-phosphate synthase, arginine-specific, large chain:arginine-specific carbamoyl-phosphate synthetase, ammonia chain] [gn:cpa2:j2002] [gtcf:5.1:6.6]
CONTIG4268	25489007_f3_6	4050	18153	567	189	YJR109C	648	9.1(10)-63	Saccharomyces cerevisiae	[ui:yjr109c] [pn:arginine-specific carbamoylphosphate synthase, large chain:carbamoyl-phosphate synthase, arginine-specific, large chain:arginine-specific carbamoyl-phosphate synthetase, ammonia chain] [gn:cpa2:j2002] [gtcf:5.1:6.6]
CONTIG2939	24414187_c1_6	4051	18154	1056	352	YOR168W	702	2.3(10)-69	Saccharomyces cerevisiae	[ui:yor168w] [pn:glutaminyl-trna synthetase:glutamine--trna ligase:ghrs] [gn:gln4:o3601] [gtcf:5.1:10.6] [ec:6.1.1.18] [keggfc:5.1:10.1:10.2] [sgdfc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5381	16097902_fl_1	4052	18155	1104	368	YOR168W	1165	2.1(10)-118	Saccharomyces cerevisiae	[ui:yor168w] [pn:glutaminyl-trna synthetase:glutamine--trna ligase:ghrs] [gn:gln4:o3601] [gtcf:5.1:10.6] [ec:6.1.1.18] [keggfc:5.1:10.1:10.2] [sgdfc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1083	93792_f1_1	4053	18156	417	139	YOR303W	387	5.7(10)-36	Saccharomyces cerevisiae	[ui:yor303w] [pn:arginine-specific carbamoylphosphate synthase, small chain:carbamoyl-phosphate synthase, arginine-specific, small chain:arginine-specific carbamoyl-phosphate synthetase, glutamine chain:cps-a] [gn:cpa1] [gtcf:5.1:6.6]
CONTIG75	14273513_f3_1	4054	18157	726	242	YOR303W	787	2.3(10)-78	Saccharomyces cerevisiae	[ui:yor303w] [pn:arginine-specific carbamoylphosphate synthase, small chain:carbamoyl-phosphate synthase, arginine-specific, small chain:arginine-specific carbamoyl-phosphate synthetase, glutamine chain:cps-a] [gn:cpa1] [gtcf:5.1:6.6]
CONTIG4941	26692285_f2_2	4055	18158	1452	484	YPL091W	1521	4.0(10)-156	Saccharomyces cerevisiae	[ui:ypl091w] [pn:nadph:glutathione reductase:gr:grase] [gn:glr1:1pg17w] [gtcf:5.1:6.16:12.12] [ec:1.6.4.2] [keggf:5.1:6.9] [sgdf:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG908	32460831_f2_1	4056	18159	897	299	YGL017W	479	1.0(10)-45	Saccharomyces cerevisiae	[ui:ygl017w] [pn:arginyl tma transferase:arginyl-tma--protein transferase:arginyltransferase] [gn:ate1] [gtcf:5.1:10.11:10.7:14.1] [ec:2.3.2.8] [keggf:14.1] [sgdf:1.5:6.3:0.6.5:1:9.2.0] [db:gtc-saccharomyces cerevisiae]

b9x13k22.x	488281_fl_1	4057	18160	729	243	YKL157W	826	1.8(10)-82	Saccharomyces cerevisiae	[ui:ykl157w] [pn:aminopeptidase yscii:aminopeptidase ii:yscii] [gn:ape2:lapi:ykl611] [gtcf:5.1:10.7] [ec:3.4.11.-] [keggf:14.1] [sgdf:1.1:5.6:3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3633	11760287_fl_1	4058	18161	573	191	YPR069C	699	5.0(10)-69	Saccharomyces cerevisiae	[ui:ypr069c] [pn:putrescine aminopropyltransferase:spermidine synthase] [gn:spe3] [gtcf:5.1] [keggf:14.2] [sgdf:1.1:5] [db:gtc-saccharomyces cerevisiae]
CONTIG4615	34179753_f3_8	4059	18162	453	151	YPR069C	519	6.0(10)-50	Saccharomyces cerevisiae	[ui:ypr069c] [pn:putrescine aminopropyltransferase:spermidine synthase] [gn:spe3] [gtcf:5.1] [keggf:14.2] [sgdf:1.1:5] [db:gtc-saccharomyces cerevisiae]
CONTIG3281	4098375_fl_2	4060	18163	1044	348	YPR069C	767	3.1(10)-76	Saccharomyces cerevisiae	[ui:ypr069c] [pn:putrescine aminopropyltransferase:spermidine synthase] [gn:spe3] [gtcf:5.1] [keggf:14.2] [sgdf:1.1:5] [db:gtc-saccharomyces cerevisiae]
CONTIG5804	3212575_c2_53	4061	18164	996	332	YER023W	580	2.1(10)-56	Saccharomyces cerevisiae	[ui:yer023w] [pn:delta 1-pyrroline-5-carboxylate reductase:pyrroline-5-carboxylate reductase:p5cr:p5c reductase] [gn:pro3:ore2] [gtcf:5.10:5.16:6.6] [ec:1.5.1.2] [keggf:5.10:5.16] [sgdf:1.1:1:9.2.0] [db:gtc-saccharomyces cerevisiae]

b9x11y87.y	36367205_c2_1	4062	18165	546	182	YER087W	465	3.2(10)-44	Saccharomyces cerevisiae	[ui:yer087w] [pn:similarity to e.coli prolyl-tRNA synthetase:putative prolyl-tRNA synthetase yer087w:proline--tRNA ligase:prors] [gtcf:5.10:10.6] [ec:6.1.1.15] [keggfc:5.10:10.1:10.2] [sgdfc:5.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5287	24411686_c1_5	4063	18166	1503	501	YHR018C	1811	7.4(10)-187	Saccharomyces cerevisiae	[ui:yhr018c] [pn:arginosuccinate lyase:argininosuccinate lyase:arginosuccinase:asal] [gn:arg4] [gtcf:5.10:5.16:5.2:6.6] [ec:4.3.2.1] [keggfc:5.2:5.10:5.16] [sgdfc:1.1:1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5186	16836660_c3_18	4064	18167	2082	694	YHR020W	2134	4.4(10)-221	Saccharomyces cerevisiae	[ui:yhr020w] [pn:strong similarity to human glutamyl-prolyl-tRNA synthetase and fruit fly multifunctional aminoacyl-tRNA synthetase:putative prolyl-tRNA synthetase yhr020w:proline--tRNA ligase:prors] [gtcf:5.10:10.6] [ec:6.1.1.15] [k
CONTIG5595	4068753_c3_15	4065	18168	1062	354	YJL088W	1062	1.7(10)-107	Saccharomyces cerevisiae	[ui:yjl088w] [pn:ornithine carbamoyltransferase:otc] [gn:arg3:j0924] [gtcf:5.10:5.16:6.6] [ec:2.1.3.3] [keggfc:5.10:5.16] [sgdfc:1.1:1:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5176	12141552_f3_4	4066	18169	1275	425	YOL052C	694	1.7(10)-68	Saccharomyces cerevisiae	[ui:yol052c] [pn:adenosylmethionine decarboxylase precursor:s- adenosylmethionine decarboxylase proenzym:adometdc] [gn:spe2:o1275] [gtcf:5.10:12.12:12.15:12.8] [ec:4.1.1.50] [keggfc:5.10] [sgdfc:3.1.0:3.4.0:1.1.3.0] [db:gtc- saccharomy
CONTIG3628	4961801_c1_2	4067	18170	1017	339	YBR248C	903	1.2(10)-90	Saccharomyces cerevisiae	[ui:ybr248c] [pn:glutamine amidotransferase/cyclase:histidine biosynthesis bifunctional amidotransferase / cyclase] [gn:his7:ybr1640] [gtcf:5.1:6.6] [ec:2.4.2.-] [keggfc:5.11] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG11	14267186_c3_3	4068	18171	645	215	YCL030C	777	2.7(10)-77	Saccharomyces cerevisiae	[ui:ycl030c] [pn:phosphoribosyl- amp cyclohydrolase/phosphoribosyl-atp pyrophosphatase/histidinol dehydrogenase:phosphoribosyl-amp cyclohydrolase / phosphoribosyl-atp pyrophosphohydrolase / histidinol dehydrogenase:hdh] [gn:his4:ycl30c]

CONTIG39	11727013_f1_1	4069	18172	549	183	YCL030C	590	1.8(10)-57	Saccharomyces cerevisiae	[ui:ycl030c] [pn:phosphoribosyl-amp cyclohydrolase/phosphoribosyl-atp pyrophosphatase/histidinol dehydrogenase:phosphoribosyl-amp cyclohydrolase / phosphoribosyl-atp pyrophosphohydrolase / histidinol dehydrogenase:hdh] [gn:his4:ycl30c:
CONTIG640	20117067_f2_1	4070	18173	603	201	YCL030C	335	1.8(10)-29	Saccharomyces cerevisiae	[ui:ycl030c] [pn:phosphoribosyl-amp cyclohydrolase/phosphoribosyl-atp pyrophosphatase/histidinol dehydrogenase:phosphoribosyl-amp cyclohydrolase / phosphoribosyl-atp pyrophosphohydrolase / histidinol dehydrogenase:hdh] [gn:his4:ycl30c:
CONTIG640	24245950_f3_2	4071	18174	486	162	YCL030C	397	4.0(10)-36	Saccharomyces cerevisiae	[ui:ycl030c] [pn:phosphoribosyl-amp cyclohydrolase/phosphoribosyl-atp pyrophosphatase/histidinol dehydrogenase:phosphoribosyl-amp cyclohydrolase / phosphoribosyl-atp pyrophosphohydrolase / histidinol dehydrogenase:hdh] [gn:his4:ycl30c:

CONTIG1055	21603188_f3_3	4072	18175	396	132	YER055C	338	9.0(10)-31	Saccharomyces cerevisiae	[ui:yer055c] [pn:atp phosphoribosyltransferase] [gn:his1] [gtcf:5.11:6.6:10.2] [ec:2.4.2.17] [keggfc:5.11] [sgdfe:1.1:1.1.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5523	26384828_f3_11	4073	18176	471	157	YER055C	427	3.3(10)-40	Saccharomyces cerevisiae	[ui:yer055c] [pn:atp phosphoribosyltransferase] [gn:his1] [gtcf:5.11:6.6:10.2] [ec:2.4.2.17] [keggfc:5.11] [sgdfe:1.1:1.1.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5186	22379577_f2_2	4074	18177	957	319	YFR025C	609	1.7(10)-59	Saccharomyces cerevisiae	[ui:yfr025c] [pn:histidinol phosphate:histidinol-phosphatase] [gn:his2] [gtcf:5.11:6.6] [ec:3.1.3.15] [keggfc:5.11] [sgdfe:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3249	21492151_c3_6	4075	18178	474	158	YIL116W	346	1.3(10)-31	Saccharomyces cerevisiae	[ui:yil116w] [pn:histidinol-phosphate aminotransferase:imidazole acetol-phosphate transaminase] [gn:his5] [gtcf:5.11:6.6] [ec:2.6.1.9] [keggfc:5.11] [sgdfe:1.1.1] [db:gtc-saccharomyces cerevisiae]
blx10611.y	3944090_f2_1	4076	18179	324	108	YIL116W	205	3.6(10)-16	Saccharomyces cerevisiae	[ui:yil116w] [pn:histidinol-phosphate aminotransferase:imidazole acetol-phosphate transaminase] [gn:his5] [gtcf:5.11:6.6] [ec:2.6.1.9] [keggfc:5.11] [sgdfe:1.1.1] [db:gtc-saccharomyces cerevisiae]

CONTIG691	23831588_c2_2	4077	18180	432	144	YMR283C	143	4.0(10)-9	Saccharomyces cerevisiae	[ui:ymr283c] [pn:tma a64-2"-o-ribosylphosphate transferase:initiator tma phosphoribosyl-transferase] [gn:rit1:ym8021] [gicfc:5.11:10.6] [ec:2.4.2.-] [keggfc:5.11] [sgdgc:4.6.0] [db:gtc-saccharomyces cerevisiae]
b3x16442.x	29955088_f2_1	4078	18181	216	72	YMR283C	172	3.0(10)-12	Saccharomyces cerevisiae	[ui:ymr283c] [pn:tma a64-2"-o-ribosylphosphate transferase:initiator tma phosphoribosyl-transferase] [gn:rit1:ym8021] [gicfc:5.11:10.6] [ec:2.4.2.-] [keggfc:5.11] [sgdgc:4.6.0] [db:gtc-saccharomyces cerevisiae]
b3x16442.x	4804701_f2_2	4079	18182	408	136	YMR283C	116	3.2(10)-6	Saccharomyces cerevisiae	[ui:ymr283c] [pn:tma a64-2"-o-ribosylphosphate transferase:initiator tma phosphoribosyl-transferase] [gn:rit1:ym8021] [gicfc:5.11:10.6] [ec:2.4.2.-] [keggfc:5.11] [sgdgc:4.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3477	10742187_f3_5	4080	18183	1545	515	YPR033C	1727	5.9(10)-178	Saccharomyces cerevisiae	[ui:yp033c] [pn:histidine--tma ligase, mitochondrial:histidyl-tma synthetase, mitochondrial precursor:histidine--tma ligase:hisrs] [gn:hts1:yp9367] [gicfc:5.11:10.1:10.2:10.6] [ec:6.1.1.21] [keggfc:5.11:10.1:10.2] [sgdgc:5.4.0:9.2]

CONTIG1853	33383541_f3_1	4081	18184	1074	358	YER125W	387	5.0(10)-35	Saccharomyces cerevisiae	[ui:yer125w] [pn:ubiquitin-protein ligase:rsp5 protein] [gn:rsp5:npl1:sygp-orf41] [gtcfc:5.14:5.9:10.11:10.7:11.1:12.1 5:13.2] [ec:6.3.2.-] [keggfc:5.9:5.14] [sgdgc:3.4:0:6.3:0:6.5:1:9:1.0:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3384	11853377_f3_6	4082	18185	702	234	YER125W	373	1.6(10)-33	Saccharomyces cerevisiae	[ui:yer125w] [pn:ubiquitin-protein ligase:rsp5 protein] [gn:rsp5:npl1:sygp-orf41] [gtcfc:5.14:5.9:10.11:10.7:11.1:12.1 5:13.2] [ec:6.3.2.-] [keggfc:5.9:5.14] [sgdgc:3.4:0:6.3:0:6.5:1:9:1.0:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3384	14276538_fl_2	4083	18186	267	89	YER125W	272	1.2(10)-22	Saccharomyces cerevisiae	[ui:yer125w] [pn:ubiquitin-protein ligase:rsp5 protein] [gn:rsp5:npl1:sygp-orf41] [gtcfc:5.14:5.9:10.11:10.7:11.1:12.1 5:13.2] [ec:6.3.2.-] [keggfc:5.9:5.14] [sgdgc:3.4:0:6.3:0:6.5:1:9:1.0:11.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4226	20798943_c3_11	4084	18187	1395	465	YER125W	2064	4.9(10)-218	Saccharomyces cerevisiae	[ui:yer125w] [pn:ubiquitin-protein ligase:rsp5 protein] [gn:rsp5:np11:sygp-orf41] [gtcf:5.14:5.9:10.11:10.7:11.1:12.15:13.2] [ec:6.3.2.-] [keggfc:5.9:5.14] [sgdfc:3.4.0:6.3.0:6.5.1:9.1.0:11.1.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG901	597177_f3_3	4085	18188	333	111	YER125W	207	1.1(10)-15	Saccharomyces cerevisiae	[ui:yer125w] [pn:ubiquitin-protein ligase:rsp5 protein] [gn:rsp5:np11:sygp-orf41] [gtcf:5.14:5.9:10.11:10.7:11.1:12.15:13.2] [ec:6.3.2.-] [keggfc:5.9:5.14] [sgdfc:3.4.0:6.3.0:6.5.1:9.1.0:11.1.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3410	21882942_c1_8	4086	18189	465	155	YHR068W	509	6.9(10)-49	Saccharomyces cerevisiae	[ui:yhr068w] [pn:deoxyhypusine synthase] [gn:dys1] [gtcf:5.14:6.6] [ec:1.5.1.-] [keggfc:5.14] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4466	7073431_f2_3	4087	18190	630	210	YHR068W	662	4.2(10)-65	Saccharomyces cerevisiae	[ui:yhr068w] [pn:deoxyhypusine synthase] [gn:dys1] [gtcf:5.14:6.6] [ec:1.5.1.-] [keggfc:5.14] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5378	24417330_f1_1	4088	18191	1527	509	YBR166C	1480	8.8(10)-152	Saccharomyces cerevisiae	[ui:ybr166c] [pn:prephenate dehydrogenase:nadp+-prdh] [gn:tyr1:ybr1218] [gtcf:5.15:6.6] [ec:1.3.1.13] [keggfc:5.15] [sgdfc:1.1.1:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3412	14642827_c2_4	4089	18192	1113	371	YBR249C	1135	3.2(10)-115	Saccharomyces cerevisiae	[ui:ybr249c] [pn:2-dehydro-3-deoxyphosphoheptonate aldolase, tyrosine-inhibited:phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited:phospho-2-keto-3-deoxyheptonate aldolase:dahp synthetase:3-deoxy-d-arabino-heptulosonate 7-
CONTIG245	867061_f2_1	4090	18193	537	179	YDR035W	694	1.7(10)-68	Saccharomyces cerevisiae	[ui:ydr035w] [pn:2-dehydro-3-deoxyphosphoheptonate aldolase, phenylalanine- inhibited:phospho-2-dehydro-3-deoxyheptonate aldolase, phenylalanine-inhibited:phospho-2-keto-3-deoxyheptonate aldolase:dahp synthetase:3-deoxy-d-arabino-heptu
b9x11u19.y	12324218_c1_3	4091	18194	435	145	YDR035W	156	8.3(10)-11	Saccharomyces cerevisiae	[ui:ydr035w] [pn:2-dehydro-3-deoxyphosphoheptonate aldolase, phenylalanine- inhibited:phospho-2-dehydro-3-deoxyheptonate aldolase, phenylalanine-inhibited:phospho-2-keto-3-deoxyheptonate aldolase:dahp synthetase:3-deoxy-d-arabino-heptu

CONTIG2409	31878755_fl_1	4092	18195	828	276	YDR127W	695	2.6(10)-67	Saccharomyces cerevisiae	[ui:ydr127w] [pn:arom pentafunctional enzyme:pentafunctional arom polypeptide:contains:3- dehydroquinase synthase , 3- dehydroquinase dehydratase:3- dehydroquinase, shikimate 5- dehydrogenase , shikimate kinase , and epsp synthase] [gn:ar
CONTIG539	16281957_f3_1	4093	18196	801	267	YDR127W	663	6.7(10)-64	Saccharomyces cerevisiae	[ui:ydr127w] [pn:arom pentafunctional enzyme:pentafunctional arom polypeptide:contains:3- dehydroquinase synthase , 3- dehydroquinase dehydratase:3- dehydroquinase, shikimate 5- dehydrogenase , shikimate kinase , and epsp synthase] [gn:ar
CONTIG359	20437904_c2_3	4094	18197	1266	422	YDR127W	1384	1.3(10)-141	Saccharomyces cerevisiae	[ui:ydr127w] [pn:arom pentafunctional enzyme:pentafunctional arom polypeptide:contains:3- dehydroquinase synthase , 3- dehydroquinase dehydratase:3- dehydroquinase, shikimate 5- dehydrogenase , shikimate kinase , and epsp synthase] [gn:ar
CONTIG2181	20833425_c2_5	4095	18198	1140	380	YDR354W	539	1.7(10)-61	Saccharomyces cerevisiae	[ui:ydr354w] [pn:anthranilate phosphoribosyltransferase] [gn:trp4:d9476] [gicfc:5.15:6.6] [ec:2.4.2.18] [keggfc:5.15] [sgdfc:1.1:9.2.0] [db:gtc- saccharomyces cerevisiae]

CONTIG3009	10392192_c3_7	4096	18199	906	302	YER090W	1123	5.9(10)-114	Saccharomyces cerevisiae	[ui:yer090w] [pn:anthranilate synthase component i] [gn:trp2] [gdcfc:5.15:6.9.12] [ec:4.1.3.27] [keggfc:5.15:9.13] [sgdgc:1.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5248	14647587_c3_10	4097	18200	651	217	YER090W	471	7.2(10)-45	Saccharomyces cerevisiae	[ui:yer090w] [pn:anthranilate synthase component i] [gn:trp2] [gdcfc:5.15:6.9.12] [ec:4.1.3.27] [keggfc:5.15:9.13] [sgdgc:1.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG724	35194191_c2_3	4098	18201	942	314	YFL022C	652	4.7(10)-64	Saccharomyces cerevisiae	[ui:yfl022c] [pn:phenylalanine--tma ligase beta chain, cytosolic:phenylalanyl-tma synthetase beta chain cytoplasmic:phenylalanine--tma ligase beta chain] [gn:frs2] [gdcfc:5.15:10.6] [ec:6.1.1.20] [keggfc:5.15:10.1:10.2] [sgdgc:5.4.
CONTIG5535	129161_c2_15	4099	18202	1080	360	YGL148W	1135	3.2(10)-115	Saccharomyces cerevisiae	[ui:ygl148w] [pn:chorismate synthase:5-enolpyruvylshikimate-3-phosphate phospholyase] [gn:aro2] [gdcfc:5.15:6.6] [ec:4.6.1.4] [keggfc:5.15] [sgdgc:1.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5464	24033510_f2_7	4100	18203	288	96	YGL148W	146	1.1(10)-9	Saccharomyces cerevisiae	[ui:ygl148w] [pn:chorismate synthase:5-enolpyruvylshikimate-3-phosphate phospholyase] [gn:aro2] [gdcfc:5.15:6.6] [ec:4.6.1.4] [keggfc:5.15] [sgdgc:1.1:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5088	14188317_f2_1	4101	18204	1644	548	YGL026C	2224	1.3(10)-230	Saccharomyces cerevisiae	[ui:ygl026c] [pn:tryptophan synthase] [gn:trp5] [gtcf:5.15:6.6] [ec:4.2.1.20] [keggc:5.15] [sgdfc:1.1.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3493	24331527_f3_2	4102	18205	1038	346	YGR185C	1228	4.4(10)-125	Saccharomyces cerevisiae	[ui:ygr185c] [pn:tyrosyl-tma synthetase:tyrosyl-tma synthetase, cytoplasmic:tyrosyl--tma ligase:tyrrs] [gn:tysl:mgm104:g7522] [gtcf:5.15:10.6] [ec:6.1.1.1] [keggc:5.15:10.1:10.2] [sgdfc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevisi]
CONTIG712	197291_c3_5	4103	18206	324	108	YGR185C	148	7.2(10)-10	Saccharomyces cerevisiae	[ui:ygr185c] [pn:tyrosyl-tma synthetase:tyrosyl-tma synthetase, cytoplasmic:tyrosyl--tma ligase:tyrrs] [gn:tysl:mgm104:g7522] [gtcf:5.15:10.6] [ec:6.1.1.1] [keggc:5.15:10.1:10.2] [sgdfc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevisi]
CONTIG2552	195312_f3_4	4104	18207	1050	350	YKL211C	799	1.3(10)-79	Saccharomyces cerevisiae	[ui:ykl211c] [pn:anthranilate synthase component ii:contains:glutamine amidotransferase:indole-3-glycerol phosphate synthase:prai] [gn:trp3] [gtcf:5.15:6.6:9.12] [keggc:5.15:9.13] [sgdfc:1.1.1:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG735	2914843_c1_3	4105	18208	285	95	YKL211C	203	1.1(10)-15	Saccharomyces cerevisiae	[ui:ykl211c] [pn:anthranilate synthase component ii:contains:glutamine amidotransferase:indole-3-glycerol phosphate synthase:prai] [gn:trp3] [gtcfc:5.15:6.9:12] [keggfc:5.15:9.13] [sgdfc:1.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2916	9877291_f2_1	4106	18209	723	241	YLR060W	781	1.0(10)-77	Saccharomyces cerevisiae	[ui:yrlr060w] [pn:phenylalanyl-trna synthetase, alpha subunit, cytosolic:phenylalanyl-trna synthetase alpha chain cytoplasmic:phenylalanine--trna ligase alpha chain:phers] [gn:frs1:12165] [gtcfc:5.15:10.6] [ec:6.1.1.20] [keggfc:5.15:10]
CONTIG2916	22690962_f2_2	4107	18210	258	86	YLR060W	278	1.3(10)-23	Saccharomyces cerevisiae	[ui:yrlr060w] [pn:phenylalanyl-trna synthetase, alpha subunit, cytosolic:phenylalanyl-trna synthetase alpha chain cytoplasmic:phenylalanine--trna ligase alpha chain:phers] [gn:frs1:12165] [gtcfc:5.15:10.6] [ec:6.1.1.20] [keggfc:5.15:10]
CONTIG5007	9879376_f3_5	4108	18211	807	269	YLR060W	879	4.2(10)-88	Saccharomyces cerevisiae	[ui:yrlr060w] [pn:phenylalanyl-trna synthetase, alpha subunit, cytosolic:phenylalanyl-trna synthetase alpha chain cytoplasmic:phenylalanine--trna ligase alpha chain:phers] [gn:frs1:12165] [gtcfc:5.15:10.6] [ec:6.1.1.20] [keggfc:5.15:10]

CONTIG5142	24398452_f3_3	4109	18212	801	267	YNL316C	237	8.0(10)-30	Saccharomyces cerevisiae	[ui:ynl316c] [pn:prephenate dehydratase:pdh] [gn:pha2:n0351] [gtcf:5.15:6.6] [ec:4.2.1.51] [keggfc:5.15] [sgdfe:1.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5677	16582932_c3_27	4110	18213	948	316	YPR060C	807	1.8(10)-80	Saccharomyces cerevisiae	[ui:ypr060c] [pn:chorismate mutase:cm] [gn:aro7:osm2:yp9499] [gtcf:5.15:6.6] [ec:5.4.99.5] [keggfc:5.15] [sgdfe:1.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5792	4788128_f1_4	4111	18214	1281	427	YDR300C	1190	4.7(10)-121	Saccharomyces cerevisiae	[ui:ydr300c] [pn:glutamate 5-kinase:gamma-glutamyl kinase:gk] [gn:pro1:d9740] [gtcf:5.16:6.6] [ec:2.7.2.11] [keggfc:5.16] [sgdfe:1.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1365	789078_c3_2	4112	18215	849	283	YOR323C	781	1.0(10)-77	Saccharomyces cerevisiae	[ui:yor323c] [pn:gamma-glutamyl phosphate reductase:gpr:glutamate-5-semialdehyde dehydrogenase:glutamyl-gamma-semialdehyde dehydrogenase] [gn:pro2:o6155] [gtcf:5.16:6.9.10] [ec:1.2.1.41] [keggfc:5.16:9.10] [sgdfe:1.1.1] [db:gtc-sa]

CONTIG3268	21675425_f3_4	4113	18216	327	109	YOR323C	150	5.7(10)-10	Saccharomyces cerevisiae	[ui:yor323c] [pn:gamma-glutamyl phosphate reductase:gpr:glutamate-5-semialdehyde dehydrogenase:glutamyl-gamma-semialdehyde dehydrogenase] [gn:pro2:o6155] [gtcf:5.16:6.9.10] [ec:1.2.1.41] [keggfc:5.16:9.10] [sgdfc:1.1.1] [db:gtc-sa]
CONTIG4888	36516688_f1_1	4114	18217	963	321	YHR019C	836	9.3(10)-90	Saccharomyces cerevisiae	[ui:yhr019c] [pn:asparaginy-l-trna-synthetase:putative asparaginy-l-trna synthetase:asparagine-- tma ligase:asnrs] [gn:ded81] [gtcf:5.2:10.6] [ec:6.1.1.22] [keggfc:5.2:10.1:10.2] [sgdfc:5.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4888	2766578_f3_3	4115	18218	654	218	YHR019C	887	6.0(10)-89	Saccharomyces cerevisiae	[ui:yhr019c] [pn:asparaginy-l-trna-synthetase:putative asparaginy-l-trna synthetase:asparagine-- tma ligase:asnrs] [gn:ded81] [gtcf:5.2:10.6] [ec:6.1.1.22] [keggfc:5.2:10.1:10.2] [sgdfc:5.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4106	53942_c1_5	4116	18219	564	188	YLL018C	741	1.8(10)-73	Saccharomyces cerevisiae	[ui:yll018c] [pn:aspartyl-tma synthetase, cytosolic:aspartyl-tma synthetase, cytoplasmic:aspartate-- tma ligase:asprs] [gn:dpsl:apsl:aps:11295] [gtcf:5.2:10.6] [ec:6.1.1.12] [keggfc:5.2:10.1:10.2] [sgdfc:5.4.0:9.2.0] [db:gtc-saccha]

CONTIG4495	21751587_t2_2	4117	18220	1221	407	YLL018C	741	1.8(10)-73	Saccharomyces cerevisiae	[ui:yll018c] [pn:aspartyl-tRNA synthetase, cytosolic:aspartyl-tRNA synthetase, cytoplasmic:aspartate--tRNA ligase:asprs] [gn:dpsl:apsl:aps:11295] [gtcf:5.2:10.6] [ec:6.1.1.12] [keggfc:5.2:10.1:10.2] [sgdfc:5.4.0.9.2.0] [db:gtc-saccha
CONTIG2325	26172812_c3_4	4118	18221	372	124	YOR335C	327	2.0(10)-28	Saccharomyces cerevisiae	[ui:yor335c] [pn:alanyl-tRNA synthetase, cytosolic:alanyl-tRNA synthetase, cytoplasmic:alanine--tRNA ligase:alars] [gn:ala1] [gtcf:5.2:10.6:11.1] [ec:6.1.1.7] [keggfc:5.2:10.1:10.2] [sgdfc:5.4.0.9.1.0] [db:gtc-saccharomyces cerevisia
CONTIG2325	25656942_c3_3	4119	18222	300	100	YOR335C	180	1.1(10)-12	Saccharomyces cerevisiae	[ui:yor335c] [pn:alanyl-tRNA synthetase, cytosolic:alanyl-tRNA synthetase, cytoplasmic:alanine--tRNA ligase:alars] [gn:ala1] [gtcf:5.2:10.6:11.1] [ec:6.1.1.7] [keggfc:5.2:10.1:10.2] [sgdfc:5.4.0.9.1.0] [db:gtc-saccharomyces cerevisia
CONTIG4725	25572577_c2_5	4120	18223	1452	484	YOR335C	1566	6.7(10)-161	Saccharomyces cerevisiae	[ui:yor335c] [pn:alanyl-tRNA synthetase, cytosolic:alanyl-tRNA synthetase, cytoplasmic:alanine--tRNA ligase:alars] [gn:ala1] [gtcf:5.2:10.6:11.1] [ec:6.1.1.7] [keggfc:5.2:10.1:10.2] [sgdfc:5.4.0.9.1.0] [db:gtc-saccharomyces cerevisia

b9x12989.y	11751013_c3_3	4121	18224	531	177	YOR335C	621	3.2(10)-60	Saccharomyces cerevisiae	[ui:yor335c] [pn:alanyl-trna synthetase, cytosolic:alanyl-trna synthetase, cytoplasmic:alanine--trna ligase:alars] [gn:ala1] [gtcf:5.2:10.6:1.1] [ec:6.1.1.7] [keggf:5.2:10.1:10.2] [sgdfc:5.4.0.9.1.0] [db:gtc-saccharomyces cerevisiae]
b2x13837.x	20912902_c3_2	4122	18225	444	148	YBR121C	408	1.2(10)-37	Saccharomyces cerevisiae	[ui:ybr121c] [pn:glycyl-trna synthetase:glycine--trna ligase:glyrs] [gn:grs1:ybr0917] [gtcf:5.3:10.6] [ec:6.1.1.14] [keggf:5.3:10.1:10.2] [sgdfc:5.4.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2090	5870969_c1_4	4123	18226	1386	462	YBR121C	1357	9.5(10)-139	Saccharomyces cerevisiae	[ui:ybr121c] [pn:glycyl-trna synthetase:glycine--trna ligase:glyrs] [gn:grs1:ybr0917] [gtcf:5.3:10.6] [ec:6.1.1.14] [keggf:5.3:10.1:10.2] [sgdfc:5.4.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4690	34398402_f3_3	4124	18227	1122	374	YCL064C	520	4.7(10)-50	Saccharomyces cerevisiae	[ui:ycl064c] [pn:l-serine/l-threonine deaminase:catabolic l-serine dehydratase:l-serine deaminase / l-threonine dehydratase:l-threonine deaminase] [gn:cha1:ycl64c] [gtcf:5.3:5.5] [keggf:5.3:5.5] [sgdfc:1.1.4] [db:gtc-saccharomyces cerevisiae]

CONTIG5213	4687875_f2_6	4125	18228	1164	388	YCL064C	435	4.7(10)-41	Saccharomyces cerevisiae	[ui:ycl064c] [pn:l-serine/l-threonine deaminase:catabolic l-serine dehydratase:l-serine deaminase / l-threonine dehydratase:l-threonine deaminase] [gn:cha1:ycl64c] [gtcf:5.3:5.5] [keggf:5.3:5.5] [sgdf:1.1:4] [db:gtc-saccharomyces cerevisiae]
CONTIG1064	12926676_f2_1	4126	18229	531	177	YCR053W	530	4.0(10)-51	Saccharomyces cerevisiae	[ui:ycr053w] [pn:o-p-homoserine p-lyase:threonine synthase] [gn:thr4:ycr53w] [gtcf:5.3:6.6:9.3] [ec:4.2.99.2] [keggf:5.3:9.3] [sgdf:1.1:1:9.2:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3063	12926676_f3_2	4127	18230	303	101	YCR053W	243	5.7(10)-20	Saccharomyces cerevisiae	[ui:ycr053w] [pn:o-p-homoserine p-lyase:threonine synthase] [gn:thr4:ycr53w] [gtcf:5.3:6.6:9.3] [ec:4.2.99.2] [keggf:5.3:9.3] [sgdf:1.1:1:9.2:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5366	30603762_f1_1	4128	18231	1071	357	YCR053W	1123	5.9(10)-114	Saccharomyces cerevisiae	[ui:ycr053w] [pn:o-p-homoserine p-lyase:threonine synthase] [gn:thr4:ycr53w] [gtcf:5.3:6.6:9.3] [ec:4.2.99.2] [keggf:5.3:9.3] [sgdf:1.1:1:9.2:0] [db:gtc-saccharomyces cerevisiae]

CONTIG1772	1562_f2_2	4129	18232	1077	359	YDR023W	1242	1.5(10)-126	Saccharomyces cerevisiae	[ui:ydr023w] [pn:seryl-tRNA synthetase, cytosolic:seryl-tRNA ligase:serr] [gn:ses1.sers:ydr9813] [gtcf:5.3:10.6] [ec:6.1.1.11] [keggfc:5.3:10.1:10.2] [sgdfc:5.4.0:9.2.0] [db:gtc-saccharomyces cer
CONTIG4014	34197502_c2_9	4130	18233	774	258	YDR158W	878	5.4(10)-88	Saccharomyces cerevisiae	[ui:ydr158w] [pn:aspartate-semialdehyde dehydrogenase:asa dh] [gn:hom2.ydr8358] [gtcf:5.3:5.8:6.6] [ec:1.2.1.11] [keggfc:5.3:5.8] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG533	859627_f1_1	4131	18234	324	108	YDR158W	295	3.2(10)-26	Saccharomyces cerevisiae	[ui:ydr158w] [pn:aspartate-semialdehyde dehydrogenase:asa dh] [gn:hom2.ydr8358] [gtcf:5.3:5.8:6.6] [ec:1.2.1.11] [keggfc:5.3:5.8] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4049	10548137_c1_3	4132	18235	1647	549	YER052C	1470	1.0(10)-150	Saccharomyces cerevisiae	[ui:yer052c] [pn:l-aspartate 4-phosphate:aspartokinase:aspartate kinase] [gn:hom3] [gtcf:5.3:5.8:6.6] [ec:2.7.2.4] [keggfc:5.3:5.8] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]

CONTIG2043	14563786_c2_4	4133	18236	633	211	YER081W	787	2.3(10)-78	Saccharomyces cerevisiae	[ui:yer081w] [pn:strong similarity to phosphoglycerate dehydrogenases:putative d-3-phosphoglycerate dehydrogenase yer081w:pgdh] [gtcf:5.3:6.6] [ec:1.1.1.95] [keggfc:5.3] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4919	2930192_f3_5	4134	18237	183	61	YER081W	119	1.3(10)-6	Saccharomyces cerevisiae	[ui:yer081w] [pn:strong similarity to phosphoglycerate dehydrogenases:putative d-3-phosphoglycerate dehydrogenase yer081w:pgdh] [gtcf:5.3:6.6] [ec:1.1.1.95] [keggfc:5.3] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5749	24414063_c3_24	4135	18238	1557	519	YGR155W	981	6.5(10)-99	Saccharomyces cerevisiae	[ui:ygr155w] [pn:cystathionine beta-synthase:serine sulphydrase:beta-thionase] [gn:cys4:str4:g6667] [gtcf:5.3:5.4:6.4:6.6] [ec:4.2.1.22] [keggfc:5.3:5.4:6.4] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4612	3960825_fl_1	4136	18239	603	201	YGR208W	532	2.5(10)-51	Saccharomyces cerevisiae	[ui:ygr208w] [pn:phosphoserine phosphatase:o-phosphoserine phosphohydrolase:psp] [gn:ser2:g7744] [gtcf:5.3:6.3:6.6] [ec:3.1.3.3] [keggfc:5.3] [sgdfc:1.1.1:16.0.0] [db:gtc-saccharomyces cerevisiae]

b3x16033.y	11855379_c2_4	4137	18240	738	246	YGR208W	118	6.4(10)-5	Saccharomyces cerevisiae	[ui:YGR208w] [pn:phosphoserine phosphatase:o-phosphoserine phosphohydrolase:psp] [gn:ser2:g7744] [gtcf:5.3:6.6] [ec:3.1.3.3] [keggf:5.3] [sgdf:1.1:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5780	14876562_c3_38	4138	18241	288	96	YHR011W	227	2.2(10)-18	Saccharomyces cerevisiae	[ui:YHR011w] [pn:seryl-tRNA synthetase:putative seryl-tRNA synthetase YHR011w:serine--tRNA ligase:serr] [gtcf:5.3:10.6] [ec:6.1.1.11] [keggf:5.3:10.1:10.2] [sgdf:5.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5780	25635056_c2_32	4139	18242	1296	432	YHR011W	768	2.5(10)-76	Saccharomyces cerevisiae	[ui:YHR011w] [pn:seryl-tRNA synthetase:putative seryl-tRNA synthetase YHR011w:serine--tRNA ligase:serr] [gtcf:5.3:10.6] [ec:6.1.1.11] [keggf:5.3:10.1:10.2] [sgdf:5.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3817	10937590_fl_1	4140	18243	1194	398	YHR025W	981	6.5(10)-99	Saccharomyces cerevisiae	[ui:YHR025w] [pn:homoserine kinase:hk] [gn:thr1] [gtcf:5.3:6.6] [ec:2.7.1.39] [keggf:5.3] [sgdf:1.1.1] [db:gtc-saccharomyces cerevisiae]

CONTIG1776	4803801_fl_1	4141	18244	312	104	YIL078W	219	4.7(10)-17	Saccharomyces cerevisiae	[ui:yil078w] [pn:threonyl tma synthetase, cytosolic:threonyl-tma synthetase, cytoplasmic:threonine--trna ligase:thrs] [gn:ths1] [gtcf:5.3:10.6] [ec:6.1.1.3] [keggfc:5.3:10.1:10.2] [sgdfc:5.4.0.9.2.0] [db:gtc-saccharomyces cerevisi]
CONTIG3658	16972257_c2_11	4142	18245	813	271	YIL078W	865	1.3(10)-86	Saccharomyces cerevisiae	[ui:yil078w] [pn:threonyl tma synthetase, cytosolic:threonyl-tma synthetase, cytoplasmic:threonine--trna ligase:thrs] [gn:ths1] [gtcf:5.3:10.6] [ec:6.1.1.3] [keggfc:5.3:10.1:10.2] [sgdfc:5.4.0.9.2.0] [db:gtc-saccharomyces cerevisi]
CONTIG3658	35429656_c1_9	4143	18246	1068	356	YIL078W	1331	5.4(10)-136	Saccharomyces cerevisiae	[ui:yil078w] [pn:threonyl tma synthetase, cytosolic:threonyl-tma synthetase, cytoplasmic:threonine--trna ligase:thrs] [gn:ths1] [gtcf:5.3:10.6] [ec:6.1.1.3] [keggfc:5.3:10.1:10.2] [sgdfc:5.4.0.9.2.0] [db:gtc-saccharomyces cerevisi]
CONTIG5160	24306512_fl_2	4144	18247	1083	361	YJR139C	1083	1.0(10)-109	Saccharomyces cerevisiae	[ui:yjr139c] [pn:homoserine dehydrogenase:hdh] [gn:hom6;2132] [gtcf:5.3:5.8:6.6] [ec:1.1.1.3] [keggfc:5.3:5.8] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]

CONTIG3353	33382660_f2_1	4145	18248	1197	399	YOR184W	1140	9.4(10)-116	Saccharomyces cerevisiae	[ui:yor184w] [pn:phosphoserine transaminase:phosphoserine aminotransferase] [gn:ser1:serc] [gtcf:5.3:6.6:9.10:9.11:9.3] [ec:2.6.1.52] [keggf:5.3:9.3] [sgdfc:1.1.1:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3295	782752_f3_4	4146	18249	582	194	YAL044C	351	3.7(10)-32	Saccharomyces cerevisiae	[ui:yal044c] [pn:strong similarity to human glycine cleavage system protein h:glycine cleavage system h protein precursor] [gn:gev3:fun40] [gtcf:5.3] [keggf:14.2] [sgdfc:1.1.4] [db:gtc-saccharomyces cerevisiae]
CONTIG2235	16287662_f1_1	4147	18250	1284	428	YBR006W	1007	1.2(10)-101	Saccharomyces cerevisiae	[ui:ybr006w] [pn:strong similarity to e.coli succinate semialdehyde dehydrogenase:hypothetical aldehyde-dehydrogenase like protein in coq1 - hhfl intergenic region] [gn:ybr0112] [gtcf:5.3] [keggf:14.2] [sgdfc:1.1.4] [db:gtc-saccharom]
CONTIG4997	15041078_c3_4	4148	18251	1464	488	YBR006W	1251	1.6(10)-127	Saccharomyces cerevisiae	[ui:ybr006w] [pn:strong similarity to e.coli succinate semialdehyde dehydrogenase:hypothetical aldehyde-dehydrogenase like protein in coq1 - hhfl intergenic region] [gn:ybr0112] [gtcf:5.3] [keggf:14.2] [sgdfc:1.1.4] [db:gtc-saccharom]
CONTIG5770	33985702_f3_12	4149	18252	807	269	YDR272W	665	2.0(10)-65	Saccharomyces cerevisiae	[ui:ydr272w] [pn:glyoxalase ii:hydroxyacylglutathione hydrolase] [gn:glo2] [gtcf:5.3] [keggf:14.2] [sgdfc:1.1.4] [db:gtc-saccharomyces cerevisiae]

CONTIG4221	16829635_c3_5	4150	18253	579	193	YDR294C	473	4.5(10)-45	Saccharomyces cerevisiae	[ui:ydr294c] [pn:similarity to glutamate decarboxylases] [gtcf:5.3] [keggf:14.2] [sgdgc:1.1.4] [db:gtc-saccharomyces cerevisiae]
CONTIG4387	3937762_f3_3	4151	18254	1263	421	YDR294C	1007	1.2(10)-101	Saccharomyces cerevisiae	[ui:ydr294c] [pn:similarity to glutamate decarboxylases] [gtcf:5.3] [keggf:14.2] [sgdgc:1.1.4] [db:gtc-saccharomyces cerevisiae]
CONTIG5700	9940637_f2_6	4152	18255	1173	391	YDR502C	1390	3.0(10)-142	Saccharomyces cerevisiae	[ui:ydr502c] [pn:s-adenosylmethionine synthetase 2:methionine adenosyltransferase 2:adomet synthetase 2] [gn:sam2:eth2:d9719] [gtcf:5.3:5.4:6.4] [ec:2.5.1.6] [keggf:5.4:6.4] [sgdgc:1.1.4] [db:gtc-saccharomyces cerevisiae]
CONTIG3645	35156338_f3_2	4153	18256	267	89	YGL202W	100	0.00016	Saccharomyces cerevisiae	[ui:ygl202w] [pn:similarity to rat kynurenine/alpha-aminoacidipate aminotransferase:hypothetical 56.2 kd protein in kex1-mcm6 intergenic region] [gtcf:5.3] [keggf:14.2] [sgdgc:1.1.4] [db:gtc-saccharomyces cerevisiae]
CONTIG5645	6250_f3_13	4154	18257	1200	400	YGL202W	1076	5.7(10)-109	Saccharomyces cerevisiae	[ui:ygl202w] [pn:similarity to rat kynurenine/alpha-aminoacidipate aminotransferase:hypothetical 56.2 kd protein in kex1-mcm6 intergenic region] [gtcf:5.3] [keggf:14.2] [sgdgc:1.1.4] [db:gtc-saccharomyces cerevisiae]

CONTIG4646	19765817_f1_1	4155	18258	1524	508	YHR137W	758	5.2(10)-81	Saccharomyces cerevisiae	[ui:yhr137w] [pn:similarity to rat kynurenine/alpha-aminoadipate aminotransferase:hypothetical 58.5 kd protein in yck1-sps100 intergenic region] [gtcf:5.3] [keggf:14.2] [sgdfc:1.1.4] [db:gtc-saccharomyces cerevisiae]
CONTIG5291	24666030_f3_8	4156	18259	624	208	YIL042C	145	4.9(10)-12	Saccharomyces cerevisiae	[ui:yil042c] [pn:similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase:hypothetical 45.4 kd protein in cbr5-not3 intergenic region] [gtcf:5.3] [keggf:14.2] [sgdfc:1.1.4] [db:gtc-saccharomyces cerevisiae]
CONTIG4157	26618825_c3_5	4157	18260	414	138	YJR025C	434	6.0(10)-41	Saccharomyces cerevisiae	[ui:yjr025c] [pn:3-hydroxyanthranilic acid dioxygenase:hypothetical 20.2 kd protein in mer2-cpr7 intergenic region] [gn:had1:j1550] [gtcf:5.3.9.10.9.11] [keggf:14.2] [sgdfc:1.1.4.1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5793	24068887_c1_16	4158	18261	1470	490	YJR078W	923	9.3(10)-93	Saccharomyces cerevisiae	[ui:yjr078w] [pn:similarity to mammalian indoleamine 2,3-dioxygenase:hypothetical 50.8 kd protein in mir1-ste18 intergenic region] [gn:j1840] [gtcf:5.3.9.10.9.11] [keggf:14.2] [sgdfc:1.1.4.1.7.1] [db:gtc-saccharomyces cerevisiae]

CONTIG2892	32657886_f1_1	4159	18262	666	222	YLR231C	570	2.3(10)-55	Saccharomyces cerevisiae	[ui:ylr231c] [pn:strong similarity to rat kynureninase] [gdcf:5.3.9.10.9.11] [keggf:14.2] [sgdcf:1.4.1.7.1] [db:gdc-saccharomyces cerevisiae]
CONTIG3178	29503250_f1_1	4160	18263	894	298	YLR231C	575	7.0(10)-56	Saccharomyces cerevisiae	[ui:ylr231c] [pn:strong similarity to rat kynureninase] [gdcf:5.3.9.10.9.11] [keggf:14.2] [sgdcf:1.4.1.7.1] [db:gdc-saccharomyces cerevisiae]
CONTIG3512	2197892_f3_6	4161	18264	1548	516	YER043C	1943	7.5(10)-201	Saccharomyces cerevisiae	[ui:yer043c] [pn:s-adenosyl-l-homocysteine hydrolase:adenosylhomocysteinease: s-adenosyl-l-homocysteine hydrolase:adocycase] [gn:sah1] [gdcf:5.4.6.4.9.10.9.11] [ec:3.3.1.1] [keggf:5.4.6.4] [sgdcf:1.7.1] [db:gdc-saccharomyces cerevisi]
CONTIG5537	7070306_f2_2	4162	18265	2310	770	YER091C	3015	0	Saccharomyces cerevisiae	[ui:yer091c] [pn:5-methyltetrahydropteroyltriglutamate --homocysteine methyltransferase:5-methyltetrahydropteroyltriglutamate --homocysteine s-methyltransferase:methionine synthase, vitamin-b12 independent isozyme:delta-p8 protein] [gn:

CONTIG5637	14954837_c2_22	4163	18266	957	319	YGR264C	1136	2.5(10)-115	Saccharomyces cerevisiae	[ui:ygr264c] [pn:methionyl-trna synthetase:methionyl-trna -trna ligase:metrs] [gn:mes1] [gtcf:5.4.6.4:10.6] [ec:6.1.1.10] [keggfc:5.4.6.4:10.1:10.2] [sgdfe:5.4.0.9.2.0] [db:gtc-saccharomyces cerevis]
CONTIG5637	34189130_c1_17	4164	18267	813	271	YGR264C	1049	4.0(10)-106	Saccharomyces cerevisiae	[ui:ygr264c] [pn:methionyl-trna synthetase:methionyl-trna -trna ligase:metrs] [gn:mes1] [gtcf:5.4.6.4:10.6] [ec:6.1.1.10] [keggfc:5.4.6.4:10.1:10.2] [sgdfe:5.4.0.9.2.0] [db:gtc-saccharomyces cerevis]
CONTIG5637	21991557_c3_27	4165	18268	528	176	YGR264C	90	0.12	Saccharomyces cerevisiae	[ui:ygr264c] [pn:methionyl-trna synthetase:methionyl-trna -trna ligase:metrs] [gn:mes1] [gtcf:5.4.6.4:10.6] [ec:6.1.1.10] [keggfc:5.4.6.4:10.1:10.2] [sgdfe:5.4.0.9.2.0] [db:gtc-saccharomyces cerevis]

CONTIG3549	25507778_f3_4	4166	18269	468	156	YNL247W	319	9.4(10)-28	Saccharomyces cerevisiae	[ui:ynl247w] [pn:similarity to cysteinyl-tma synthetases:putative c29e6.06c:cysteine-- tma ligase:cysrs] [gn:n0885] [gtcf:5.5:10.6] [ec:6.1.1.16] [keggfc:5.5:10.1:10.2] [sgdfc:5.4.0] [db:gtc-saccharomyces]
CONTIG3792	34195290_c1_9	4167	18270	225	75	YNL247W	137	3.2(10)-8	Saccharomyces cerevisiae	[ui:ynl247w] [pn:similarity to cysteinyl-tma synthetases:putative c29e6.06c:cysteine-- tma ligase:cysrs] [gn:n0885] [gtcf:5.5:10.6] [ec:6.1.1.16] [keggfc:5.5:10.1:10.2] [sgdfc:5.4.0] [db:gtc-saccharomyces]
CONTIG3792	34616436_c2_12	4168	18271	1152	384	YNL247W	1083	1.0(10)-109	Saccharomyces cerevisiae	[ui:ynl247w] [pn:similarity to cysteinyl-tma synthetases:putative c29e6.06c:cysteine-- tma ligase:cysrs] [gn:n0885] [gtcf:5.5:10.6] [ec:6.1.1.16] [keggfc:5.5:10.1:10.2] [sgdfc:5.4.0] [db:gtc-saccharomyces]

CONTIG3792	35807828_c2_11	4169	18272	348	1116	YNL247W	359	4.5(10)-32	Saccharomyces cerevisiae	[ui:ynl247w] [pn:similarity to cysteinyl-trna synthetases:putative c29e6.06c:cysteine-- trna ligase:cysrs] [gn:n0885] [gtcf:5.5:10.6] [ec:6.1.1.16] [keggfc:5.5:10.1:10.2] [sgdfc:5.4.0] [db:gtc-saccharomyces]
CONTIG5164	14470311_f3_5	4170	18273	1194	398	YJR148W	1260	1.8(10)-128	Saccharomyces cerevisiae	[ui:yjr148w] [pn:branched chain amino acid aminotransferase, cytosolic:putative branched-chain amino acid aminotransferase, cytosolic:bcat] [gn:tw2:j2209] [gtcf:5.6:5.7:6:6:9.5] [ec:2.6.1.42] [keggfc:5.6:5.7:9.5] [sgdfc:1.1:1:9.2.0]
CONTIG3500	22710078_c2_12	4171	18274	648	216	YJR148W	589	2.2(10)-57	Saccharomyces cerevisiae	[ui:yjr148w] [pn:branched chain amino acid aminotransferase, cytosolic:putative branched-chain amino acid aminotransferase, cytosolic:bcat] [gn:tw2:j2209] [gtcf:5.6:5.7:6:6:9.5] [ec:2.6.1.42] [keggfc:5.6:5.7:9.5] [sgdfc:1.1:1:9.2.0]
CONTIG1669	214583_c2_6	4172	18275	1008	336	YBL076C	1222	1.8(10)-124	Saccharomyces cerevisiae	[ui:ybl076c] [pn:isoleucyl-trna synthetase:isoleucyl-trna synthetase, cytoplasmic:isoleucine-- trna ligase:ilers] [gn:ils1:ybl0734] [gtcf:5.7:10.6] [ec:6.1.1.5] [keggfc:5.7:10.1:10.2] [sgdfc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevis]

b1x15324.x	34179687_c2_2	4173	18276	624	208	YBL076C	615	2.8(10)-59	Saccharomyces cerevisiae	[ui:ybl076c] [pn:isoleucyl-trna synthetase:isoleucyl-trna synthetase, cytoplasmic:isoleucine-- trna ligase:ilers] [gn:ils1:ybl0734] [gtcf:5.7:10.6] [ec:6.1.1.5] [keggfc:5.7:10.1:10.2] [sgdfc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevis]
CONTIG4072	11882662_f2_2	4174	18277	1137	379	YCL018W	1315	2.7(10)-134	Saccharomyces cerevisiae	[ui:ycl018w] [pn:beta-isopropyl-malate dehydrogenase:3-isopropylmalate dehydrogenase:beta-ipm dehydrogenase:imd:3-ipm-dh] [gn:leu2:ycl18w] [gtcf:5.7:6.6] [ec:1.1.1.85] [keggfc:5.7] [sgdfc:1.1:9.2.0] [db:gtc-saccharomyces cerevisia]
CONTIG3855	19553175_c2_5	4175	18278	879	293	YGL009C	1136	2.5(10)-115	Saccharomyces cerevisiae	[ui:ygl009c] [pn:3-isopropylmalate dehydratase:isopropylmalate isomerase:alpha-ipm isomerase:ipmi] [gn:leu1] [gtcf:5.7:6.6] [ec:4.2.1.33] [keggfc:5.7] [sgdfc:1.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4886	2197192_f1_1	4176	18279	1086	362	YGL009C	1146	2.2(10)-116	Saccharomyces cerevisiae	[ui:ygl009c] [pn:3-isopropylmalate dehydratase:isopropylmalate isomerase:alpha-ipm isomerase:ipmi] [gn:leu1] [gtcf:5.7:6.6] [ec:4.2.1.33] [keggfc:5.7] [sgdfc:1.1:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5739	33757812_f2_11	4177	18280	705	235	YPL160W	533	2.2(10)-50	Saccharomyces cerevisiae	[ui:yp1160w] [pn:leucine--trna ligase, cytosolic:leucyl-trna synthetase, cytoplasmic:leucine--trna ligase:leurs] [gn:cdc60:p2564] [gtcf:5.7:10.6] [ec:6.1.1.4] [keggfc:5.7:10.1:10.2] [sgdfc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevisia
CONTIG5382	11074_c1_12	4178	18281	2703	901	YPL160W	3034	0	Saccharomyces cerevisiae	[ui:yp1160w] [pn:leucine--trna ligase, cytosolic:leucyl-trna synthetase, cytoplasmic:leucine--trna ligase:leurs] [gn:cdc60:p2564] [gtcf:5.7:10.6] [ec:6.1.1.4] [keggfc:5.7:10.1:10.2] [sgdfc:5.4.0:9.2.0] [db:gtc-saccharomyces cerevisia
CONTIG3798	35203425_f1_1	4179	18282	462	154	YBR115C	375	2.8(10)-33	Saccharomyces cerevisiae	[ui:ybr115c] [pn:l-aminoadipate-semialdehyde dehydrogenase, large subunit:aminoadipate-semialdehyde dehydrogenase large subunit:alpha-aminoadipate reductase:alpha-ar] [gn:lys2:ybr0910] [gtcf:5.8:5.9:6.6] [ec:1.2.1.31] [keggfc:5.8:5.9
CONTIG5782	898450_c2_23	4180	18283	1524	508	YBR115C	1484	3.2(10)-152	Saccharomyces cerevisiae	[ui:ybr115c] [pn:l-aminoadipate-semialdehyde dehydrogenase, large subunit:aminoadipate-semialdehyde dehydrogenase large subunit:alpha-aminoadipate reductase:alpha-ar] [gn:lys2:ybr0910] [gtcf:5.8:5.9:6.6] [ec:1.2.1.31] [keggfc:5.8:5.9

CONTIG5782	34657062_c2_22	4181	18284	270	90	YBR115C	344	5.7(10)-30	Saccharomyces cerevisiae	[ui:ybr115c] [pn:l-aminoadipate-semialdehyde dehydrogenase, large subunit:aminoadipate-semialdehyde dehydrogenase large subunit:alpha-aminoadipate reductase:alpha-ar] [gn:lys2:ybr0910] [gtcf:5.8:5.9:6.6] [ec:1.2.1.31] [keggfc:5.8:5.9]
CONTIG5782	4766436_c3_27	4182	18285	2040	680	YBR115C	2034	1.7(10)-210	Saccharomyces cerevisiae	[ui:ybr115c] [pn:l-aminoadipate-semialdehyde dehydrogenase, large subunit:aminoadipate-semialdehyde dehydrogenase large subunit:alpha-aminoadipate reductase:alpha-ar] [gn:lys2:ybr0910] [gtcf:5.8:5.9:6.6] [ec:1.2.1.31] [keggfc:5.8:5.9]
CONTIG5253	10160038_c3_15	4183	18286	1824	608	YDR037W	2301	8.8(10)-239	Saccharomyces cerevisiae	[ui:ydr037w] [pn:lysyl-tma synthetase, cytosolic:lysyl-tma synthetase, cytoplasmic:lysine-- tma ligase:lysr] [gn:krs1:gcd5:yd9673] [gtcf:5.8:10.6] [ec:6.1.1.6] [keggfc:5.8:10.1:10.2] [sgdfe:5.4.0.9.2.0] [db:gtc-saccharomyces cere
CONTIG5512	4079051_c3_13	4184	18287	1167	389	YIR034C	1310	9.0(10)-134	Saccharomyces cerevisiae	[ui:yir034c] [pn:saccharopine dehydrogenase:nad+, l-lysine forming:lysine-- 2-oxoglutarate reductase:sdh] [gn:lys1] [gtcf:5.8:5.9:6.6] [ec:1.5.1.7] [keggfc:5.8:5.9] [sgdfe:1.1:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG497	953431_c2_8	4185	18288	1362	454	YNR050C	1651	6.5(10)-170	Saccharomyces cerevisiae	[ui:ynr050c] [pn:saccharopine dehydrogenase:nadp+, l-glutamate forming] [gn:lys9:lys13:n3461] [gtcf:5.8:6.6] [ec:1.5.1.10] [keggf:5.8] [sgdf:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4907	25_f2_3	4186	18289	1380	460	YER078C	984	3.2(10)-99	Saccharomyces cerevisiae	[ui:yer078c] [pn:hypothetical 58.0 kd peptidase in arg5,6-ilv1 intergenic region] [gtcf:5.9] [ec:3.4.-.-] [keggf:5.9] [db:gtc-saccharomyces cerevisiae]
CONTIG4907	14880002_f3_6	4187	18290	234	78	YER078C	150	7.0(10)-10	Saccharomyces cerevisiae	[ui:yer078c] [pn:hypothetical 58.0 kd peptidase in arg5,6-ilv1 intergenic region] [gtcf:5.9] [ec:3.4.-.-] [keggf:5.9] [db:gtc-saccharomyces cerevisiae]
CONTIG2338	565888_f3_5	4188	18291	495	165	YFR006W	496	1.6(10)-47	Saccharomyces cerevisiae	[ui:yfr006w] [pn:similarity to x-pro dipeptidases:hypothetical 61.8 kd peptidase in mpr1-gcn20 intergenic region] [gtcf:5.9:10.11] [ec:3.4.-.-] [keggf:5.9] [sgdf:6.5.3] [db:gtc-saccharomyces cerevisiae]
CONTIG4924	24238407_f3_7	4189	18292	534	178	YIR022W	522	2.8(10)-50	Saccharomyces cerevisiae	[ui:yir022w] [pn:signal sequence processing protein:signal sequence processing protein precursor] [gn:sec11] [gtcf:1.1:5.9:10.7] [ec:3.4.-.-] [keggf:5.9] [sgdf:6.3:0.9:4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5159	10600952_c3_8	4190	18293	951	317	YIL145C	711	2.7(10)-70	Saccharomyces cerevisiae	[ui:yil145c] [pn:similarity to e.coli pantothenate synthetase:putative pantoate--beta-alanine ligase:pantothenate synthetase:pantoate activating enzyme] [gtcf:6.1:9.10:9.11:9.5] [ec:6.3.2.1] [keggfc:6.1:9.5] [sgdfc:1.7.1] [db:gtc-sac]
CONTIG4551	19723132_c1_11	4191	18294	540	180	YBR244W	461	8.4(10)-44	Saccharomyces cerevisiae	[ui:ybr244w] [pn:strong similarity to glutathione peroxidases:glutathione peroxidase homolog ybr244w] [gn:ybr1632] [gtcf:6.16:12.12] [ec:1.11.1.9] [keggfc:6.9] [sgdfc:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3600	1379006_f2_1	4192	18295	282	94	YIR037W	260	1.7(10)-22	Saccharomyces cerevisiae	[ui:yir037w] [pn:glutathione peroxidase] [gn:hyl1] [gtcf:6.16:13.2] [ec:1.11.1.9] [keggfc:6.9] [sgdfc:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5098	4100133_c1_10	4193	18296	699	233	YIR037W	480	8.0(10)-46	Saccharomyces cerevisiae	[ui:yir037w] [pn:glutathione peroxidase] [gn:hyl1] [gtcf:6.16:13.2] [ec:1.11.1.9] [keggfc:6.9] [sgdfc:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5098	1953502_c3_11	4194	18297	579	193	YIR037W	644	3.3(10)-63	Saccharomyces cerevisiae	[ui:yir037w] [pn:glutathione peroxidase] [gn:hyl1] [gtcf:6.16:13.2] [ec:1.11.1.9] [keggfc:6.9] [sgdfc:11.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5401	812932_c1_11	4195	18298	474	158	YAL016W	197	9.6(10)-19	Saccharomyces cerevisiae	[ui:yal016w] [pn:ser/thr protein phosphatase 2a, regulatory chain a:protein phosphatase pp2a regulatory subunit a:pr65] [gn:tpd3:fun32] [gtcf:6.3:10.2:12.8] [keggfc:14.2] [sgdfc:3.1.0.3.2.0.3.8.0.3.9.0.4.12.0:16.0.0] [db:gtc-saccharo
CONTIG5401	24806578_c1_10	4196	18299	1104	368	YAL016W	965	3.2(10)-97	Saccharomyces cerevisiae	[ui:yal016w] [pn:ser/thr protein phosphatase 2a, regulatory chain a:protein phosphatase pp2a regulatory subunit a:pr65] [gn:tpd3:fun32] [gtcf:6.3:10.2:12.8] [keggfc:14.2] [sgdfc:3.1.0.3.2.0.3.8.0.3.9.0.4.12.0:16.0.0] [db:gtc-saccharo
CONTIG5401	24495287_c3_16	4197	18300	447	149	YAL016W	439	2.1(10)-41	Saccharomyces cerevisiae	[ui:yal016w] [pn:ser/thr protein phosphatase 2a, regulatory chain a:protein phosphatase pp2a regulatory subunit a:pr65] [gn:tpd3:fun32] [gtcf:6.3:10.2:12.8] [keggfc:14.2] [sgdfc:3.1.0.3.2.0.3.8.0.3.9.0.4.12.0:16.0.0] [db:gtc-saccharo
b1x17840.x	25867876_f2_1	4198	18301	753	251	YBL056W	296	5.0(10)-26	Saccharomyces cerevisiae	[ui:ybl056w] [pn:ser/thr protein phosphatase pp2c:putative 51.4 kd intergenic region] [gn:pic3:ybl0511:ybl0513] [gtcf:6.3:14.3] [ec:3.1.3.16] [keggfc:14.1] [sgdfc:16.0.0:13.0.0] [db:gtc-saccharomyces cere

CONTIG1970	4771931_c1_3	4199	18302	297	99	YBR125C	171	2.2(10)-12	Saccharomyces cerevisiae	[ui:ybr125c] [pn:similarity to protein phosphatase 2c:putative 44.2 kd phosphatase 2c in tfc1-cif1 intergenic region] [gn:ybr0921] [gtcf:6.3:14.3] [ec:3.1.3.16] [keggf:14.1] [sgdfc:16.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
b3x10869.x	14973516_f3_1	4200	18303	504	168	YBR125C	266	3.8(10)-23	Saccharomyces cerevisiae	[ui:ybr125c] [pn:similarity to protein phosphatase 2c:putative 44.2 kd phosphatase 2c in tfc1-cif1 intergenic region] [gn:ybr0921] [gtcf:6.3:14.3] [ec:3.1.3.16] [keggf:14.1] [sgdfc:16.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1257	23629675_f1_1	4201	18304	807	269	YBR276C	117	0.00042	Saccharomyces cerevisiae	[ui:ybr276c] [pn:protein tyrosine phosphatase:probable protein-tyrosine phosphatase ybr276c] [gn:pps1:ybr2013] [gtcf:6.3:12.8] [ec:3.1.3.48] [keggf:14.1] [sgdfc:3.8.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4090	23609443_c2_3	4202	18305	2202	734	YBR276C	326	6.7(10)-44	Saccharomyces cerevisiae	[ui:ybr276c] [pn:protein tyrosine phosphatase:probable protein-tyrosine phosphatase ybr276c] [gn:pps1:ybr2013] [gtcf:6.3:12.8] [ec:3.1.3.48] [keggf:14.1] [sgdfc:3.8.0:16.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2457	4881312_f3_2	4203	18306	597	199	YBR276C	177	1.8(10)-12	Saccharomyces cerevisiae	[ui:ybr276c] [pn:protein tyrosine phosphatase:probable protein-tyrosine phosphatase ybr276c] [gn:pps1:ybr2013] [gtcf:6.3:12.8] [ec:3.1.3.48] [keggfc:14.1] [sgdfc:3.8.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5770	14502005_f1_7	4204	18307	1122	374	YDL230W	432	9.9(10)-41	Saccharomyces cerevisiae	[ui:ydl230w] [pn:protein tyrosine phosphatase:protein-tyrosine phosphatase 1:ptpase 1] [gn:ptp1] [gtcf:6.3:12.8:14.3] [ec:3.1.3.48] [keggfc:13.3] [sgdfc:9.2.0:16.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2672	29338333_f3_3	4205	18308	324	108	YDL188C	507	1.1(10)-48	Saccharomyces cerevisiae	[ui:ydl188c] [pn:protein ser/thr phosphatase pp2a-2:serine/threonine protein phosphatase pp2a-2 catalytic subunit] [gn:pph22:sis4:d1271] [gtcf:6.3:12.13:12.8] [ec:3.1.3.16] [keggfc:14.1] [sgdfc:1.5.2:3.1.0:3.2.0:3.8.0:16.0.0] [db:gtc]
CONTIG108	26600307_f3_1	4206	18309	816	272	YDL134C	978	1.3(10)-98	Saccharomyces cerevisiae	[ui:ydl134c] [pn:protein ser/thr phosphatase pp2a-1:serine/threonine protein phosphatase pp2a-1 catalytic subunit] [gn:pph21:d2180] [gtcf:6.3:12.13:12.8] [ec:3.1.3.16] [keggfc:13.3] [sgdfc:1.5.2:3.1.0:3.2.0:3.8.0:16.0.0] [db:gtc-sacc]

CONTIG4167	4870177_13_5	4207	18310	957	319	YDL047W	1415	6.7(10)-145	Saccharomyces cerevisiae	[ui:ydl047w] [pn:ser/thr protein phosphatase:serine/threonine protein phosphatase ppl-1] [gn:pph1:slit4:d2693] [gtcf:6.3:12.8] [ec:3.1.3.16] [keggfc:13.3] [sgdfe:3.2.0.3.8.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1118	24110300_c1_5	4208	18311	558	186	YDL006W	263	8.0(10)-23	Saccharomyces cerevisiae	[ui:ydl006w] [pn:protein serine/threonine phosphatase 2c:protein phosphatase 2c homolog:pp2c] [gn:ptc1:tpd1:d2925] [gtcf:6.3:12.13:12.8:13.2] [ec:3.1.3.16] [keggfc:14.1] [sgdfe:1.5.2.3.1.0.3.2.0:10.3.4:11.1.0:16.0.0] [db:gtc-saccharo
CONTIG5206	24110300_c3_14	4209	18312	1161	387	YDL006W	506	1.3(10)-48	Saccharomyces cerevisiae	[ui:ydl006w] [pn:protein serine/threonine phosphatase 2c:protein phosphatase 2c homolog:pp2c] [gn:ptc1:tpd1:d2925] [gtcf:6.3:12.13:12.8:13.2] [ec:3.1.3.16] [keggfc:14.1] [sgdfe:1.5.2.3.1.0.3.2.0:10.3.4:11.1.0:16.0.0] [db:gtc-saccharo
b3x15922.x	25432192_f1_1	4210	18313	552	184	YDR075W	702	2.3(10)-69	Saccharomyces cerevisiae	[ui:ydr075w] [pn:protein ser/thr phosphatase:serine/threonine protein phosphatase pph3] [gn:pph3:d4421] [gtcf:6.3:12.8] [ec:3.1.3.16] [keggfc:14.1] [sgdfe:3.1.0:16.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4514	4784651_f1_1	4211	18314	1257	419	YDR481C	681	4.0(10)-67	Saccharomyces cerevisiae	[ui:ydr481c] [pn:repressible alkaline phosphatase vacuolar:repressible alkaline phosphatase precursor] [gn:pho8] [gtcf:6.3.8.1:9.13:9.6:12.16] [ec:3.1.3.1] [keggf:8.1:9.7:9.12] [sgdfc:9.10.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5768	20288_f3_13	4212	18315	750	250	YDR481C	585	6.0(10)-57	Saccharomyces cerevisiae	[ui:ydr481c] [pn:repressible alkaline phosphatase vacuolar:repressible alkaline phosphatase precursor] [gn:pho8] [gtcf:6.3.8.1:9.13:9.6:12.16] [ec:3.1.3.1] [keggf:8.1:9.7:9.12] [sgdfc:9.10.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5768	33761050_f1_5	4213	18316	951	317	YDR481C	881	2.6(10)-88	Saccharomyces cerevisiae	[ui:ydr481c] [pn:repressible alkaline phosphatase vacuolar:repressible alkaline phosphatase precursor] [gn:pho8] [gtcf:6.3.8.1:9.13:9.6:12.16] [ec:3.1.3.1] [keggf:8.1:9.7:9.12] [sgdfc:9.10.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5657	12303452_c2_17	4214	18317	1800	600	YEL042W	1357	9.5(10)-139	Saccharomyces cerevisiae	[ui:yel042w] [pn:guanosine diphosphate:guanosine-diphosphate:gdpase] [gn:gda1:sygp-orf16] [gtcf:6.3.10.7:12.16] [ec:3.6.1.42] [keggf:14.1] [sgdfc:6.3.0:9.4.0:16.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3205	23697252_f2_1	4215	18318	1623	541	YER075C	145	3.1(10)-14	Saccharomyces cerevisiae	[ui:yer075c] [pn:protein tyrosine phosphatase:probable protein-tyrosine phosphatase yer075c] [gn:ptp3] [gicfc:6.3:14.3] [ec:3.1.3.48] [keggfc:14.1] [sgdgc:16.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG656	859383_f1_2	4216	18319	291	97	YER075C	102	0.00022	Saccharomyces cerevisiae	[ui:yer075c] [pn:protein tyrosine phosphatase:probable protein-tyrosine phosphatase yer075c] [gn:ptp3] [gicfc:6.3:14.3] [ec:3.1.3.48] [keggfc:14.1] [sgdgc:16.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG656	24095062_f1_3	4217	18320	390	130	YER075C	148	2.7(10)-9	Saccharomyces cerevisiae	[ui:yer075c] [pn:protein tyrosine phosphatase:probable protein-tyrosine phosphatase yer075c] [gn:ptp3] [gicfc:6.3:14.3] [ec:3.1.3.48] [keggfc:14.1] [sgdgc:16.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
b9x12x90.x	32527005_f3_2	4218	18321	519	173	YER075C	115	9.0(10)-6	Saccharomyces cerevisiae	[ui:yer075c] [pn:protein tyrosine phosphatase:probable protein-tyrosine phosphatase yer075c] [gn:ptp3] [gicfc:6.3:14.3] [ec:3.1.3.48] [keggfc:14.1] [sgdgc:16.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4089	1054750_c2_10	4219	18322	906	302	YER089C	294	3.6(10)-37	Saccharomyces cerevisiae	[ui:yer089c] [pn:strong similarity to phosphoprotein phosphatase 2c in seb1-trp2 intergenic region] [gn:pic2] [gtcf:6.3:14.3] [ec:3.1.3.16] [keggfc:14.1] [sgdfe:16.0:13.0.0] [db:gtc-saccharomyces cerev
CONTIG5301	21978924_c1_10	4220	18323	960	320	YER133W	1425	5.9(10)-146	Saccharomyces cerevisiae	[ui:yer133w] [pn:ser/thr phosphoprotein phosphatase 1, catalytic chain:serine/threonine protein phosphatase ppl-2] [gn:glc7:dis2:cld1] [gtcf:6.3:7.1:7.2:10.7:12.13:12.8] [ec:3.1.3.16] [keggfc:13.3] [sgdfe:1.5:2.2:7.0:3.2:0.3:5.0:3.8.
CONTIG5806	2766886_c1_26	4221	18324	1302	434	YFR028C	1232	1.7(10)-125	Saccharomyces cerevisiae	[ui:yfr028c] [pn:protein-tyrosine-phosphatase:probable protein-tyrosine phosphatase] [gn:cdc14] [gtcf:6.3:10.8:12.8] [ec:3.1.3.48] [keggfc:13.3] [sgdfe:3.6:0.3:8.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
b3x16043.y	10651905_f2_2	4222	18325	396	132	YFR028C	236	4.0(10)-19	Saccharomyces cerevisiae	[ui:yfr028c] [pn:protein-tyrosine-phosphatase:probable protein-tyrosine phosphatase] [gn:cdc14] [gtcf:6.3:10.8:12.8] [ec:3.1.3.48] [keggfc:13.3] [sgdfe:3.6:0.3:8.0:16.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1691	1365882_f3_1	4223	18326	1080	360	YGL190C	1034	1.6(10)-104	Saccharomyces cerevisiae	[ui:ygl190c] [pn:ser/thr phosphatase 2a regulatory subunit b:protein b:pr55:cell division control protein 55] [gn:cdc55:g1345] [gtcf:6.3:12.8:13.2] [keggfc:14.2] [sgdfc:3.1.0.3.2.0.3.8.0.3.9.0:11.1]
CONTIG609	190888_f3_1	4224	18327	1335	445	YGR123C	778	1.8(10)-91	Saccharomyces cerevisiae	[ui:ygr123c] [pn:protein ser/thr phosphatase:serine/threonine protein phosphatase t:ppt] [gn:ppt1:g6347] [gtcf:6.3:14.3] [ec:3.1.3.16] [keggfc:14.1] [sgdfc:16.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5670	19720377_c2_30	4225	18328	525	175	YGR203W	245	6.5(10)-21	Saccharomyces cerevisiae	[ui:ygr203w] [pn:weak similarity to x.laevis protein-tyrosin-phosphatase cdc homolog 2 and to hypothetical protein ypr200c:hypothetical 17.2 kd protein in pct1-ade3 intergenic region] [gn:g7731] [gtcf:6.3:14.3] [keggfc:14.2] [sgdfc:1]
CONTIG2121	22051912_c3_2	4226	18329	807	269	YIL002C	91	0.38	Saccharomyces cerevisiae	[ui:yil002c] [pn:synaptojanin homolog 1:hypothetical 108.4 kd protein in bet1-pan1 intergenic region] [gn:shl.yia2c] [gtcf:6.3:8.5:10.7] [keggfc:14.2] [sgdfc:1.6.7:16.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4602	9806427_f2_3	4227	18330	1053	351	YIL002C	731	2.1(10)-72	Saccharomyces cerevisiae	[ui:yil002c] [pn:synaptojanin homolog 1:hypothetical 108.4 kd protein in bet1-pan1 intergenic region] [gn:sjh1:yia2c] [gtcf:6.3:8.5:10.7] [keggfc:14.2] [sgdfc:1.6:7:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5813	24065877_c3_61	4228	18331	1080	360	YIR026C	587	3.7(10)-57	Saccharomyces cerevisiae	[ui:yir026c] [pn:protein tyrosine phosphatase:protein-tyrosine phosphatase:ptpase] [gn:yvh1] [gtcf:6.3:12.13:12.15:12.8] [ec:3.1.3.48] [keggfc:14.1] [sgdfc:3.4:0.3:5.0:10.4:7:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4689	4188540_f2_2	4229	18332	615	205	YKL190W	614	5.0(10)-60	Saccharomyces cerevisiae	[ui:ykl190w] [pn:calcineurin b, regulatory subunit:calcineurin b subunit:protein phosphatase 2b regulatory subunit] [gn:cnb1:ycnb:ycn2] [gtcf:6.3:10.2:12.9] [keggfc:14.2] [sgdfc:3.0:4.8:2.9:2.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5466	10625676_f2_4	4230	18333	888	296	YML112W	111	0.00064	Saccharomyces cerevisiae	[ui:yml112w] [pn:carboxy-terminal domain:ctd kinase, gamma subunit:ctd kinase gamma subunit:ctd kinase 32 kd subunit:ctdk-i gamma subunit] [gn:ctk3:ym8339] [gtcf:6.3:8.5:9.4:10.1:10.2] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:4.8:2:9.5.0]

CONTIG373	14884441_f3_1	4231	18334	801	267	YML016C	709	4.4(10)-70	Saccharomyces cerevisiae	[ui:yml016c] [pn:ser/thr phosphatase required for normal osmoregulation:serine/threonine protein phosphatase pp-zl] [gn:ppz1:ym9571] [gtcf:6.3:13.2] [ec:3.1.3.16] [keggf:14.1] [sgdfe:11.1.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3862	782887_c2_6	4232	18335	357	119	YML016C	543	1.7(10)-52	Saccharomyces cerevisiae	[ui:yml016c] [pn:ser/thr phosphatase required for normal osmoregulation:serine/threonine protein phosphatase pp-zl] [gn:ppz1:ym9571] [gtcf:6.3:13.2] [ec:3.1.3.16] [keggf:14.1] [sgdfe:11.1.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG210	24020939_c2_1	4233	18336	585	195	YML016C	702	2.3(10)-69	Saccharomyces cerevisiae	[ui:yml016c] [pn:ser/thr phosphatase required for normal osmoregulation:serine/threonine protein phosphatase pp-zl] [gn:ppz1:ym9571] [gtcf:6.3:13.2] [ec:3.1.3.16] [keggf:14.1] [sgdfe:11.1.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1341	25635817_f3_1	4234	18337	1107	369	YMR036C	191	9.0(10)-13	Saccharomyces cerevisiae	[ui:yml036c] [pn:m-phase inducing protein tyrosine phosphatase:m-phase inducer phosphatase:mitosis initiation protein mih1:mitotic inducer homolog] [gn:mih1:ym9532] [gtcf:6.3:12.8] [ec:3.1.3.48] [keggf:13.3] [sgdfe:3.8.0:16.0.0] [db

b1x14347.x	11775417_f3_1	4235	18338	516	172	YNL217W	172	9.8(10)-13	Saccharomyces cerevisiae	[ui:ynl217w] [pn:weak similarity to e.coli bis:5"-nucleosyl-tetraphosphatase:hypothetical 37.2 kd protein in alg9-rap1 intergenic region] [gn:n1306] [gtcf:6.3:14.3] [keggf:14.2] [sgdf:16.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
b2x18173.y	25625781_f3_1	4236	18339	474	158	YNL128W	139	1.3(10)-16	Saccharomyces cerevisiae	[ui:ynl128w] [pn:weak similarity to tensin:hypothetical 50.2 kd protein in cpl1-spc98 intergenic region] [gn:n1220:n1872] [gtcf:6.3:14.3] [keggf:14.2] [sgdf:16.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1134	3009683_f3_2	4237	18340	1056	352	YNL106C	323	7.9(10)-28	Saccharomyces cerevisiae	[ui:ynl106c] [pn:phosphatidylinositol phosphate phosphatase:hypothetical 133.3 kd protein in cyb5-leu4 intergenic region] [gn:pie3:n2160] [gtcf:6.3:10.7:11.1] [keggf:14.2] [sgdf:6.2.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2301	20441656_c2_5	4238	18341	414	138	YNL106C	262	2.5(10)-21	Saccharomyces cerevisiae	[ui:ynl106c] [pn:phosphatidylinositol phosphate phosphatase:hypothetical 133.3 kd protein in cyb5-leu4 intergenic region] [gn:pie3:n2160] [gtcf:6.3:10.7:11.1] [keggf:14.2] [sgdf:6.2.0:16.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3574	25578760_c2_9	4239	18342	2457	819	YNL106C	1651	6.5(10)-170	Saccharomyces cerevisiae	[ui:ynl106c] [pn:phosphatidylinositol phosphate phosphatase:hypothetical 133.3 kd protein in cyb5-leu4 intergenic region] [gn:pie3:n2160] [gtcf:6.3:10.7:11.1] [keggfc:14.2] [sgdfc:6.2.0:16.0.0] [db:gtc- saccharomyces cerevisiae]
CONTIG4602	25992268_f1_1	4240	18343	921	307	YNL106C	321	1.3(10)-27	Saccharomyces cerevisiae	[ui:ynl106c] [pn:phosphatidylinositol phosphate phosphatase:hypothetical 133.3 kd protein in cyb5-leu4 intergenic region] [gn:pie3:n2160] [gtcf:6.3:10.7:11.1] [keggfc:14.2] [sgdfc:6.2.0:16.0.0] [db:gtc- saccharomyces cerevisiae]
CONTIG5748	12947827_c3_25	4241	18344	783	261	YNR032W	755	5.9(10)-75	Saccharomyces cerevisiae	[ui:ynr032w] [pn:phosphoprotein phosphatase ppg catalytic chain:serine/threonine protein phosphatase pp2a-like ppg1] [gn:ppg1:ppg:n3281] [gtcf:6.3:7.1:7.2] [ec:3.1.3.16] [keggfc:14.1] [sgdfc:2.7.0:16.0.0] [db:gtc-saccharomyces cerevi]
CONTIG229	32615933_c1_2	4242	18345	330	110	YOL064C	179	2.2(10)-13	Saccharomyces cerevisiae	[ui:yol064c] [pn:protein ser/thr phosphatase:halotolerance protein hal2] [gn:hal2:mc122] [gtcf:6.3:6.6:13.2] [keggfc:14.2] [sgdfc:1.1.1:1.1.0:16.0.0] [db:gtc- saccharomyces cerevisiae]

CONTIG4182	901577_c3_8	4243	18346	876	292	YOL064C	473	4.5(10)-45	Saccharomyces cerevisiae	[ui:yol064c] [pn:protein ser/thr phosphatase:halotolerance protein hal2] [gn:hal2:met22] [gtcf:6.3:6.6:13.2] [keggfc:14.2] [sgdgc:1.1:1.1:1.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4383	901577_c2_11	4244	18347	1200	400	YOL064C	736	6.0(10)-73	Saccharomyces cerevisiae	[ui:yol064c] [pn:protein ser/thr phosphatase:halotolerance protein hal2] [gn:hal2:met22] [gtcf:6.3:6.6:13.2] [keggfc:14.2] [sgdgc:1.1:1.1:1.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5094	6120766_f3_7	4245	18348	693	231	YOL064C	383	1.5(10)-35	Saccharomyces cerevisiae	[ui:yol064c] [pn:protein ser/thr phosphatase:halotolerance protein hal2] [gn:hal2:met22] [gtcf:6.3:6.6:13.2] [keggfc:14.2] [sgdgc:1.1:1.1:1.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1548	4787511_f1_1	4246	18349	339	113	YOR007C	145	1.1(10)-9	Saccharomyces cerevisiae	[ui:yor007c] [pn:similarity to protein phosphatases] [gtcf:6.3:14.3] [keggfc:14.2] [sgdgc:16.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4573	6913441_c2_12	4247	18350	1167	389	YOR007C	115	0.00042	Saccharomyces cerevisiae	[ui:yor007c] [pn:similarity to protein phosphatases] [gtcf:6.3:14.3] [keggfc:14.2] [sgdgc:16.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5488	24429813_c1_10	4248	18351	1212	404	YOR007C	638	1.5(10)-62	Saccharomyces cerevisiae	[ui:yor007c] [pn:similarity to protein phosphatases] [gtcf:6.3:14.3] [keggfc:14.2] [sgdgc:16.0:13.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2168	9867812_c3_4	4249	18352	999	333	YOR014W	444	3.5(10)-58	Saccharomyces cerevisiae	[ui:yor014w] [pn:potential regulatory subunit of protein phosphatase 2a:rtsl protein:scsl protein] [gn:rtsl:scsl:or26] [gicfc:6.3:13.2] [keggfc:14.2] [sgdgc:9.2.0:11.1.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG641	9782594_c2_5	4250	18353	1104	368	YOR014W	978	1.3(10)-98	Saccharomyces cerevisiae	[ui:yor014w] [pn:potential regulatory subunit of protein phosphatase 2a:rtsl protein:scsl protein] [gn:rtsl:scsl:or26] [gicfc:6.3:13.2] [keggfc:14.2] [sgdgc:9.2.0:11.1.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5577	4117153_f3_6	4251	18354	1293	431	YOR090C	697	8.1(10)-69	Saccharomyces cerevisiae	[ui:yor090c] [pn:similarity to ser/thr protein phosphatases] [gicfc:6.3:14.3] [keggfc:14.2] [sgdgc:16.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3558	3913132_f3_5	4252	18355	1458	486	YOR178C	143	6.5(10)-11	Saccharomyces cerevisiae	[ui:yor178c] [pn:ser/thr phosphoprotein phosphatase 1, regulatory chain:protein phosphatase 1 regulatory subunit] [gn:gac1] [gicfc:6.3:7.1:7.2:12.13] [keggfc:14.2] [sgdgc:1.5.2.2.7.0.9.2.0:16.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4310	20034655_c3_9	4253	18356	1299	433	YOR178C	147	1.3(10)-9	Saccharomyces cerevisiae	[ui:yor178c] [pn:ser/thr phosphoprotein phosphatase 1, regulatory chain:protein phosphatase 1 regulatory subunit] [gn:gac1] [gicfc:6.3:7.1:7.2:12.13] [keggfc:14.2] [sgdgc:1.5.2.2.7.0.9.2.0:16.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1104	31542281_f3_4	4254	18357	372	124	YPL152W	111	6.4(10)-6	Saccharomyces cerevisiae	[ui:ypl152w] [pn:strong similarity to human phosphotyrosyl phosphatase activator] [gtcf:6.3:14.3] [keggf:14.2] [sgdf:16.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5596	24417532_c2_16	4255	18358	1128	376	YPL152W	931	1.3(10)-93	Saccharomyces cerevisiae	[ui:ypl152w] [pn:strong similarity to human phosphotyrosyl phosphatase activator] [gtcf:6.3:14.3] [keggf:14.2] [sgdf:16.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
b9x13g07.x	2162792_f3_1	4256	18359	510	170	YPL152W	113	3.8(10)-6	Saccharomyces cerevisiae	[ui:ypl152w] [pn:strong similarity to human phosphotyrosyl phosphatase activator] [gtcf:6.3:14.3] [keggf:14.2] [sgdf:16.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5781	5085142_f1_8	4257	18360	537	179	YPL151C	322	4.5(10)-29	Saccharomyces cerevisiae	[ui:ypl151c] [pn:strong similarity to a.thaliana prl1 and prl2 proteins] [gtcf:6.3:14.3] [keggf:14.2] [sgdf:16.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5781	35188125_f3_15	4258	18361	636	212	YPL151C	404	9.1(10)-38	Saccharomyces cerevisiae	[ui:ypl151c] [pn:strong similarity to a.thaliana prl1 and prl2 proteins] [gtcf:6.3:14.3] [keggf:14.2] [sgdf:16.0:13.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2789	24273425_f3_2	4259	18362	531	177	YPR073C	433	7.7(10)-41	Saccharomyces cerevisiae	[ui:ypr073c] [pn:protein-tyrosine-phosphatase:low molecular weight phosphotyrosine protein phosphatase:low molecular weight cytosolic acid phosphatase:ptpase] [gn:ltpl:yp9499] [gtcf:6.3.9.13.9.2:14.3] [keggfc:9.2.9.12] [sgdgc:16.0.0:
CONTIG3302	23864068_c3_4	4260	18363	267	89	YAL004W	282	7.7(10)-25	Saccharomyces cerevisiae	[ui:yal004w] [pn:strong similarity to a.klebsiana glutamate dehydrogenase:hypothetical 23.8 kd protein in ssa1-efb1 intergenic region] [gtcf:6.6] [keggfc:14.2] [sgdgc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5775	24115905_f3_15	4261	18364	195	65	YAL004W	164	2.5(10)-12	Saccharomyces cerevisiae	[ui:yal004w] [pn:strong similarity to a.klebsiana glutamate dehydrogenase:hypothetical 23.8 kd protein in ssa1-efb1 intergenic region] [gtcf:6.6] [keggfc:14.2] [sgdgc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2671	214026_f3_2	4262	18365	1113	371	YEL046C	1051	2.5(10)-106	Saccharomyces cerevisiae	[ui:yel046c] [pn:required for glycine prototrophy in shmt1 and shmt2 double mutant:gly1 protein] [gn:gly1:sygp-orf34] [gtcf:6.6] [keggfc:14.2] [sgdgc:1.1.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5415	281258_c1_12	4263	18366	1236	412	YEL046C	1003	3.1(10)-101	Saccharomyces cerevisiae	[ui:yel046c] [pn:required for glycine prototrophy in shmt1 and shmt2 double mutant:gly1 protein] [gn:gly1:sygp-orf34] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1506	9859833_f1_1	4264	18367	780	260	YEL038W	437	2.8(10)-41	Saccharomyces cerevisiae	[ui:yel038w] [pn:similarity to k.oxytoca enolase-phosphatase e-1:utr4 protein:unknown transcript 4] [gn:utr4:sygp-orf20] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5814	24015936_f2_12	4265	18368	1233	411	YGL184C	936	3.8(10)-94	Saccharomyces cerevisiae	[ui:ygl184c] [pn:similarity to arabidopsis cystathionine beta-lyase:hypothetical 51.8 kd protein in cox4-gts1 intergenic region] [gn:g1601] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG376	10830007_f1_1	4266	18369	549	183	YHR070W	246	2.5(10)-20	Saccharomyces cerevisiae	[ui:yhr070w] [pn:strong similarity to n.crassa met-10+ protein:hypothetical 56.5 kd protein in dys1-erg7 intergenic region] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3966	9821942_c2_3	4267	18370	246	82	YHR112C	195	4.4(10)-15	Saccharomyces cerevisiae	[ui:yhr112c] [pn:similarity to cystathionine gamma-synthase:hypothetical 42.4 kd protein in cdc12-orc6 intergenic region] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]

CONTIG798	2343907_f1_1	4268	18371	621	207	YHR112C	357	8.8(10)-33	Saccharomyces cerevisiae	[ui:yhr112c] [pn:similarity to cystathionine gamma-synthase:hypothetical 42.4 kd protein in cdc12-orc6 intergenic region] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3366	5370677_c2_7	4269	18372	423	141	YIL094C	406	5.7(10)-38	Saccharomyces cerevisiae	[ui:yil094c] [pn:similarity to isopropyl malate and tartrate dehydrogenases:hypothetical 40.1 kd protein in sgal-ths1 intergenic region] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5518	33782842_f2_7	4270	18373	372	124	YIL094C	238	5.2(10)-20	Saccharomyces cerevisiae	[ui:yil094c] [pn:similarity to isopropyl malate and tartrate dehydrogenases:hypothetical 40.1 kd protein in sgal-ths1 intergenic region] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5609	14625911_c3_10	4271	18374	1776	592	YJL071W	311	1.8(10)-51	Saccharomyces cerevisiae	[ui:yjl071w] [pn:acetylglutamate synthase:hypothetical 65.6 kd protein in scp160-mrp18 intergenic region] [gn:arg2:j1091:hrb574] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5161	15632643_c2_8	4272	18375	2406	802	YKL215C	1691	3.7(10)-174	Saccharomyces cerevisiae	[ui:ykl215c] [pn:similarity to p.aeruginosa hyua and hyub:hypothetical 140.4 kd protein in ural-doa1 intergenic region] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]

CONTIG3518	20089762_c3_5	4273	18376	1212	404	YKL215C	925	5.7(10)-93	Saccharomyces cerevisiae	[ui:ykl215c] [pn:similarity to p. aeruginosa hyua and hyub:hypothetical 140.4 kd protein in ura1-doa1 intergenic region] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3518	29476511_c1_4	4274	18377	423	141	YKL215C	291	2.2(10)-24	Saccharomyces cerevisiae	[ui:ykl215c] [pn:similarity to p. aeruginosa hyua and hyub:hypothetical 140.4 kd protein in ura1-doa1 intergenic region] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5714	26571932_c3_25	4275	18378	258	86	YKL215C	152	1.5(10)-9	Saccharomyces cerevisiae	[ui:ykl215c] [pn:similarity to p. aeruginosa hyua and hyub:hypothetical 140.4 kd protein in ura1-doa1 intergenic region] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5607	16052091_f3_6	4276	18379	1674	558	YKL191W	792	8.0(10)-112	Saccharomyces cerevisiae	[ui:ykl191w] [pn:diphtheria toxin resistance protein:diphtheria toxin resistance protein 2] [gn:dph2] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2518	20361312_fl_1	4277	18380	249	83	YLR172C	236	5.7(10)-20	Saccharomyces cerevisiae	[ui:ylr172c] [pn:diphthamide methyltransferase:diphthine synthase:diphthamide biosynthesis methyltransferase] [gn:dph5:19470] [gtcf:6.6] [ec:2.1.1.98] [keggf:14.1] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]

CONTIG4706	6054758_c2_10	4278	18381	987	329	YLR172C	1062	1.7(10)-107	Saccharomyces cerevisiae	[ui:ylr172c] [pn:diphthamide methyltransferase:diphthine synthase:diphthamide biosynthesis methyltransferase] [gn:dpb5:l9470] [gtcf:6.6] [ec:2.1.1.98] [keggf:14.1] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5730	4376261_fl_3	4279	18382	2046	682	YML096W	493	2.1(10)-61	Saccharomyces cerevisiae	[ui:yml096w] [pn:weak similarity to asparagine synthases] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5682	24009687_f2_9	4280	18383	1323	441	YMR062C	1158	1.2(10)-117	Saccharomyces cerevisiae	[ui:ymr062c] [pn:similarity to glutamate n-acetyltransferase] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2542	23990627_c3_7	4281	18384	561	187	YMR250W	357	2.7(10)-32	Saccharomyces cerevisiae	[ui:ymr250w] [pn:similarity to glutamate decarboxylases] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2777	9863281_fl_1	4282	18385	1170	390	YMR250W	750	2.0(10)-74	Saccharomyces cerevisiae	[ui:ymr250w] [pn:similarity to glutamate decarboxylases] [gtcf:6.6] [keggf:14.2] [sgdfc:1.1.1] [db:gtc-saccharomyces cerevisiae]

CONTIG1469	12507088_c2_5	4283	18386	540	180	YCL043C	286	1.2(10)-24	Saccharomyces cerevisiae	[ui:ycl043c] [pn:protein disulfide-isomerase precursor:protein disulfide isomerase precursor:pdi / dolichyl-diphosphooligosaccharide-protein glycotransferase:glycosylation site-binding chain:gsbp:thioredoxin-related glycoprotein 1] [gn
CONTIG2797	878430_c3_2	4284	18387	765	255	YCL043C	401	1.8(10)-37	Saccharomyces cerevisiae	[ui:yil005w] [pn:protein disulfide-isomerase precursor:protein disulfide isomerase precursor:pdi / dolichyl-diphosphooligosaccharide-protein glycotransferase:glycosylation site-binding chain:gsbp:thioredoxin-related glycoprotein 1] [gn
CONTIG2580	4085937_c1_5	4285	18388	678	226	YIL005W	222	2.1(10)-17	Saccharomyces cerevisiae	[ui:yil005w] [pn:similarity to protein disulfide isomerases:putative disulfide isomerase yil005w precursor] [gn:yia5w] [gtcfc:7.1:10.5:10.7:11.3:12.7] [ec:5.3.4.1] [keggfc:7.2] [sgdgc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3210	10626036_c1_4	4286	18389	1305	435	YIL005W	394	5.2(10)-36	Saccharomyces cerevisiae	[ui:yil005w] [pn:similarity to protein disulfide isomerases:putative disulfide isomerase yil005w precursor] [gn:yia5w] [gtcfc:7.1:10.5:10.7:11.3:12.7] [ec:5.3.4.1] [keggfc:7.2] [sgdgc:6.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5537	24414028_f3_10	4287	18390	1239	413	YBL058W	642	5.5(10)-63	Saccharomyces cerevisiae	[ui:ybl058w] [pn:potential regulatory subunit for glc7p:shp1 protein] [gn:shp1:ybl0509:ybl0515] [gtcf:7.1:7.2:10.7:12.8] [keggfc:14.2] [sgdfc:2.7.0:3.2.0:3.5.0:3.8.0:5.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4110	7047053_f2_1	4288	18391	189	63	YHR047C	93	0.0018	Saccharomyces cerevisiae	[ui:yhr047c] [pn:alanine/arginine aminopeptidase] [gn:aap1] [gtcf:7.1:7.2:12.13] [ec:3.4.11.-] [keggfc:14.1] [sgdfc:1.5.2:2.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1438	24254651_f3_1	4289	18392	927	309	YKL128C	147	4.9(10)-8	Saccharomyces cerevisiae	[ui:ykl128c] [pn:high copy suppressor of ts tps2 mutant phenotype:hypothetical 33.8 kd protein in myo3-pgm1 intergenic region] [gn:pmu1] [gtcf:7.1:7.2] [keggfc:14.2] [sgdfc:2.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5401	6250625_f1_2	4290	18393	975	325	YKL128C	298	1.6(10)-26	Saccharomyces cerevisiae	[ui:ykl128c] [pn:high copy suppressor of ts tps2 mutant phenotype:hypothetical 33.8 kd protein in myo3-pgm1 intergenic region] [gn:pmu1] [gtcf:7.1:7.2] [keggfc:14.2] [sgdfc:2.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5530	14649125_f3_7	4291	18394	996	332	YKL128C	200	1.3(10)-14	Saccharomyces cerevisiae	[ui:ykl128c] [pn:high copy suppressor of ts tps2 mutant phenotype:hypothetical 33.8 kd protein in myo3-pgm1 intergenic region] [gn:pmu1] [gtcf:7.1:7.2] [keggfc:14.2] [sgdfc:2.7.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5530	34016500_f3_8	4292	18395	1038	346	YKL128C	185	7.5(10)-21	Saccharomyces cerevisiae	[ui:ykl128c] [pn:high copy suppressor of ts tps2 mutant phenotype:hypothetical 33.8 kd protein in myo3-pgml intergenic region] [gn:pmu1] [gtcf:7.1:7.2] [keggf:14.2] [sgdfc:2.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5661	788437_f1_1	4293	18396	945	315	YKL128C	167	2.2(10)-10	Saccharomyces cerevisiae	[ui:ykl128c] [pn:high copy suppressor of ts tps2 mutant phenotype:hypothetical 33.8 kd protein in myo3-pgml intergenic region] [gn:pmu1] [gtcf:7.1:7.2] [keggf:14.2] [sgdfc:2.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5704	4772502_f3_8	4294	18397	3726	1242	YLR071C	370	2.2(10)-33	Saccharomyces cerevisiae	[ui:yhr071c] [pn:dna-directed ma polymerase ii holoenzyme subunit:glucose repression regulatory protein] [gn:rgl1] [gtcf:7.1:7.2:10.1:10.2:12.13:12.8:12.9] [keggf:14.2] [sgdfc:1.5:2.2:7.0:3.2:0.3:3.0:4.8:1.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5111	16828400_c3_14	4295	18398	1989	663	YPL240C	1621	2.1(10)-261	Saccharomyces cerevisiae	[ui:ypl240c] [pn:heat shock protein:heat shock protein hsp82] [gn:hsp82:hsp90] [gtcf:12.7:7.1:12.8:13.2] [keggf:14.2] [sgdfc:2.7.0:3.4:0.3:5.0:9.2:0:1.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3310	31551_f2_2	4296	18399	999	333	YPL031C	1029	5.4(10)-104	Saccharomyces cerevisiae	[ui:ypl031c] [pn:cyclin-dependent protein kinase:negative regulator of the pho system] [gn:pho85] [gtcf:7.1.7.2.8.5.9.4.10.1:10.2.12.13.12.8.13.10] [ec:2.7.1.-] [keggf:8.5.9.4.13.1:13.2.13.3] [sgdfc:1.4.2.2.7.0.3.8.0.9.5.0:15.0.0.1]
CONTIG208	5320387_fl_1	4297	18400	528	176	YFR019W	241	1.0(10)-18	Saccharomyces cerevisiae	[ui:yfr019w] [pn:probable pip 5-kinase:probable phosphatidylinositol-4-phosphate 5-kinase:1-phosphatidylinositol-4-phosphate kinase:pip5k:ptdins:4p-5-kinase:diphosphoinositide kinase] [gn:fab1] [gtcf:8.1:12.16] [ec:2.7.1.68] [keggf]
CONTIG1509	26367036_f3_2	4298	18401	999	333	YFR019W	93	0.41999	Saccharomyces cerevisiae	[ui:yfr019w] [pn:probable pip 5-kinase:probable phosphatidylinositol-4-phosphate 5-kinase:1-phosphatidylinositol-4-phosphate kinase:pip5k:ptdins:4p-5-kinase:diphosphoinositide kinase] [gn:fab1] [gtcf:8.1:12.16] [ec:2.7.1.68] [keggf]
CONTIG3834	4943878_c2_2	4299	18402	1362	454	YFR019W	345	4.5(10)-58	Saccharomyces cerevisiae	[ui:yfr019w] [pn:probable pip 5-kinase:probable phosphatidylinositol-4-phosphate 5-kinase:1-phosphatidylinositol-4-phosphate kinase:pip5k:ptdins:4p-5-kinase:diphosphoinositide kinase] [gn:fab1] [gtcf:8.1:12.16] [ec:2.7.1.68] [keggf]

CONTIG5376	5861626_f2_3	4300	18403	2544	848	YFR019W	158	3.8(10)-7	Saccharomyces cerevisiae	[ui:yfr019w] [pn:probable pip 5-kinase:probable phosphatidylinositol-4-phosphate 5-kinase:1-phosphatidylinositol-4-phosphate kinase:pi5k:ptdins:4p-5-kinase:diphosphoinositide kinase] [gn:fab1] [gtcf:8.1:12.16] [ec:2.7.1.68] [keggf]
CONTIG5617	33347143_f3_4	4301	18404	966	322	YFR019W	941	3.3(10)-93	Saccharomyces cerevisiae	[ui:yfr019w] [pn:probable pip 5-kinase:probable phosphatidylinositol-4-phosphate 5-kinase:1-phosphatidylinositol-4-phosphate kinase:pi5k:ptdins:4p-5-kinase:diphosphoinositide kinase] [gn:fab1] [gtcf:8.1:12.16] [ec:2.7.1.68] [keggf]
CONTIG78	433332_f2_1	4302	18405	675	225	YFR019W	253	1.2(10)-22	Saccharomyces cerevisiae	[ui:yfr019w] [pn:probable pip 5-kinase:probable phosphatidylinositol-4-phosphate 5-kinase:1-phosphatidylinositol-4-phosphate kinase:pi5k:ptdins:4p-5-kinase:diphosphoinositide kinase] [gn:fab1] [gtcf:8.1:12.16] [ec:2.7.1.68] [keggf]

CONTIG4117	15679688_c1_2	4303	18406	1887	629	YLR305C	805	7.2(10)-79	Saccharomyces cerevisiae	[ui:ylr305c] [pn:phosphatidylinositol-4-kinase:phosphatidylinositol 4-kinase stt4:pi4-kinase:ptdins-4-kinase] [gn:stt4:l2142] [gtcf:8.1:12.13:12.8] [ec:2.7.1.67] [keggfc:8.1] [sgdfc:3.8.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4365	956942_f2_1	4304	18407	2136	712	YLR305C	1599	2.2(10)-164	Saccharomyces cerevisiae	[ui:ylr305c] [pn:phosphatidylinositol-4-kinase:phosphatidylinositol 4-kinase stt4:pi4-kinase:ptdins-4-kinase] [gn:stt4:l2142] [gtcf:8.1:12.13:12.8] [ec:2.7.1.67] [keggfc:8.1] [sgdfc:3.8.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1188	35792166_f1_1	4305	18408	1059	353	YNL267W	322	8.5(10)-28	Saccharomyces cerevisiae	[ui:ynl267w] [pn:phosphatidylinositol 4-kinase:phosphatidylinositol 4-kinase pik1:pi4-kinase:ptdins-4-kinase] [gn:pik1:n0795] [gtcf:8.1:10.1:10.2:12.13:12.8] [ec:2.7.1.67] [keggfc:8.1] [sgdfc:3.9.0:9.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2802	15712757_f3_4	4306	18409	522	174	YNL267W	294	8.4(10)-25	Saccharomyces cerevisiae	[ui:ynl267w] [pn:phosphatidylinositol 4-kinase:phosphatidylinositol 4-kinase pik1:pi4-kinase:ptdins-4-kinase] [gn:pik1:n0795] [gtcf:8.1:10.1:10.2:12.13:12.8] [ec:2.7.1.67] [keggfc:8.1] [sgdgc:3.9.0:9.5.0:15.0.0] [db:gtc-saccharomyces
CONTIG2673	25407718_f2_1	4307	18410	852	284	YNL267W	986	2.0(10)-99	Saccharomyces cerevisiae	[ui:ynl267w] [pn:phosphatidylinositol 4-kinase:phosphatidylinositol 4-kinase pik1:pi4-kinase:ptdins-4-kinase] [gn:pik1:n0795] [gtcf:8.1:10.1:10.2:12.13:12.8] [ec:2.7.1.67] [keggfc:8.1] [sgdgc:3.9.0:9.5.0:15.0.0] [db:gtc-saccharomyces
CONTIG2911	33254626_f1_1	4308	18411	939	313	YNL267W	991	5.7(10)-100	Saccharomyces cerevisiae	[ui:ynl267w] [pn:phosphatidylinositol 4-kinase:phosphatidylinositol 4-kinase pik1:pi4-kinase:ptdins-4-kinase] [gn:pik1:n0795] [gtcf:8.1:10.1:10.2:12.13:12.8] [ec:2.7.1.67] [keggfc:8.1] [sgdgc:3.9.0:9.5.0:15.0.0] [db:gtc-saccharomyces

b1x18076.x	5322766_f1_1	4309	18412	516	172	YNL267W	385	1.5(10)-34	Saccharomyces cerevisiae	[ui:ynl267w] [pn:phosphatidylinositol 4-kinase:phosphatidylinositol 4-kinase:pik1:pi4-kinase:pidins-4-kinase] [gn:pik1:n0795] [gtcf:8.1:10.1:10.2:12.13:12.8] [ec:2.7.1.67] [keggfc:8.1] [sgdfc:3.9:0.9:5.0:15.0.0] [db:gtc-saccharomyces]
b9x12575.y	25969162_c1_2	4310	18413	558	186	YNL267W	156	4.5(10)-10	Saccharomyces cerevisiae	[ui:ynl267w] [pn:phosphatidylinositol 4-kinase:phosphatidylinositol 4-kinase:pik1:pi4-kinase:pidins-4-kinase] [gn:pik1:n0795] [gtcf:8.1:10.1:10.2:12.13:12.8] [ec:2.7.1.67] [keggfc:8.1] [sgdfc:3.9:0.9:5.0:15.0.0] [db:gtc-saccharomyces]
CONTIG5297	22460307_c1_12	4311	18414	1356	452	YAR018C	397	2.6(10)-71	Saccharomyces cerevisiae	[ui:yar018c] [pn:ser/thr protein kinase:serine/threonine-protein kinase kin3] [gn:kin3:mpk1:fun52] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0:0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5233	34251566_c3_14	4312	18415	1206	402	YAR019C	605	2.1(10)-58	Saccharomyces cerevisiae	[ui:yar019c] [pn:protein kinase of the map kinase kinase kinase family:cell division control protein 15] [gn:cdc15] [gtcf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4:13.3] [sgdfc:3.8:0:15.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3766	33990918_c3_6	4313	18416	576	192	YBL105C	647	1.3(10)-62	Saccharomyces cerevisiae	[ui:ybl105c] [pn:ser/thr-specific protein kinase:protein kinase c-like 1:pkc 1] [gn:pkc1:stt1:hpo2:ybl0807] [gtcf:8.5:9.4:12.13:12.8:13.2] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:3.2.0:3.8.0:10.2.5:11.1.0:15.0.0] [db:gtc-saccharomyces c
CONTIG3284	24806563_c1_3	4314	18417	1122	374	YBL016W	974	3.7(10)-98	Saccharomyces cerevisiae	[ui:ybl016w] [pn:mitogen-activated protein kinase:map kinase:mitogen-activated protein kinase fus3:map kinase fus3] [gn:fus3:dac2:ybl0303:ybl03] [gtcf:8.5:9.4:12.13:12.8:12.9] [ec:2.7.1.-] [keggfc:8.5:9.4:13.1] [sgdfc:3.3.0:3.8.0:9.2
b1x18255.x	6814506_c2_1	4315	18418	468	156	YBL016W	517	9.8(10)-50	Saccharomyces cerevisiae	[ui:ybl016w] [pn:mitogen-activated protein kinase:map kinase:mitogen-activated protein kinase fus3:map kinase fus3] [gn:fus3:dac2:ybl0303:ybl03] [gtcf:8.5:9.4:12.13:12.8:12.9] [ec:2.7.1.-] [keggfc:8.5:9.4:13.1] [sgdfc:3.3.0:3.8.0:9.2
CONTIG5604	10553135_f3_5	4316	18419	897	299	YBR028C	287	9.3(10)-25	Saccharomyces cerevisiae	[ui:ybr028c] [pn:similarity to ribosomal protein kinases:probable serine/threonine-protein kinase ybr028c] [gn:ybr0312] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5604	34070937_f2_4	4317	18420	870	290	YBR028C	343	1.3(10)-40	Saccharomyces cerevisiae	[ui:ybr028c] [pn:similarity to ribosomal protein kinases:probable serine/threonine-protein kinase ybr028c] [gn:ybr0312] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3320	9772750_f2_2	4318	18421	627	209	YBR059C	485	3.2(10)-45	Saccharomyces cerevisiae	[ui:ybr059c] [pn:similarity to ser/thr-specific protein kinase pak1p:probable serine/threonine-protein kinase ybr059c] [gn:ybr0519] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces c
CONTIG5051	3957063_f1_1	4319	18422	1608	536	YBR059C	352	3.2(10)-29	Saccharomyces cerevisiae	[ui:ybr059c] [pn:similarity to ser/thr-specific protein kinase pak1p:probable serine/threonine-protein kinase ybr059c] [gn:ybr0519] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces c
CONTIG1377	29567590_c2_3	4320	18423	1146	382	YBR097W	538	1.3(10)-50	Saccharomyces cerevisiae	[ui:ybr097w] [pn:ser/thr protein kinase:protein kinase vps15] [gn:vps15:ybr0825] [gtcf:8.5:9.4:10.7:11.1:12.10:12.13] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:6.2.0:8.3.0:8.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1705	33635052_f2_1	4321	18424	1377	459	YBR097W	173	1.0(10)-10	Saccharomyces cerevisiae	[ui:ybr097w] [pn:ser/thr protein kinase:protein kinase vps15] [gn:vps15:ybr0825] [gicfc:8.5:9.4:10.7:11.1:12.10:12.13] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdgc:6.2.0:8.3.0:8.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5403	24789827_f1_4	4322	18425	1056	352	YBR097W	700	6.0(10)-68	Saccharomyces cerevisiae	[ui:ybr097w] [pn:ser/thr protein kinase:protein kinase vps15] [gn:vps15:ybr0825] [gicfc:8.5:9.4:10.7:11.1:12.10:12.13] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdgc:6.2.0:8.3.0:8.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4705	4475912_f2_3	4323	18426	993	331	YBR160W	1202	2.5(10)-122	Saccharomyces cerevisiae	[ui:ybr160w] [pn:cyclin-dependent protein kinase:cell division control protein 28] [gn:cdc28:srm5:ybr1211] [gicfc:8.5:9.4:10.8:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4:13.1:13.2:13.3] [sgdgc:3.2.0:3.6.0:3.8.0:15.0.0] [db:gtc-saccharom]
CONTIG5495	803161_c2_16	4324	18427	1932	644	YCR008W	1313	4.4(10)-134	Saccharomyces cerevisiae	[ui:ycr008w] [pn:similarity to npr1p and hal5p protein kinases:probable serine/threonine-protein kinase ycr8w] [gn:sat4:ycr8w:ycr101:ycr046] [gicfc:8.5:9.4:12.13:13.2] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdgc:11.1.0:15.0.0] [db:gtc-saccha]

CONTIG4031	4772782_f1_1	4325	18428	1044	348	YDL108W	1142	5.7(10)-116	Saccharomyces cerevisiae	[ui:ydl108w] [pn:cyclin-dependent ser/thr protein kinase:serine/threonine-protein kinase kin28] [gn:kin28:d2330] [gtcf:8.5:9.4:10.1:10.10:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:3.8.0:4.8.1:9.5.0:11.2.1:15.0.0] [db:gtc-
b9x11x80.x	24227342_c2_2	4326	18429	309	103	YDL101C	219	2.3(10)-17	Saccharomyces cerevisiae	[ui:ydl101c] [pn:protein kinase:dna damage response protein kinase dun1] [gn:dun1:d2370] [gtcf:8.5:9.4:10.1:10.10:10.2:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4:13.3] [sgdfc:9.5.0:11.2.1:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1961	14569708_c3_4	4327	18430	1143	381	YDL028C	411	1.0(10)-37	Saccharomyces cerevisiae	[ui:ydl028c] [pn:serine/threonine/tyrosine protein kinase:serine/threonine protein kinase mpk1:regulatory cell proliferation kinase 1] [gn:mpk1:d2785] [gtcf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:3.5.0:3.8.0:15

CONTIG2279	1269534_c1_4	4328	18431	636	212	YDL028C	536	1.1(10)-51	Saccharomyces cerevisiae	[ui:ydl028c] [pn:serine/threonine/tyrosine protein kinase:serine/threonine protein kinase mpst:regulatory cell proliferation kinase 1] [gn:mpst:rpkl:d2785] [gtcf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:3.5:0.3.8.0:15]
CONTIG2710	34182902_f3_2	4329	18432	1380	460	YDL017W	525	6.9(10)-75	Saccharomyces cerevisiae	[ui:ydl017w] [pn:protein kinase:cell division control protein 7] [gn:cdc7:oa2:d2855] [gtcf:8.5:9.4:10.1:10.2:10.8:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4:13.2] [sgdfc:3.5:0.3.6.0:3.8.0:9.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3789	16432842_f3_3	4330	18433	501	167	YDL017W	94	0.00073	Saccharomyces cerevisiae	[ui:ydl017w] [pn:protein kinase:cell division control protein 7] [gn:cdc7:oa2:d2855] [gtcf:8.5:9.4:10.1:10.2:10.8:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4:13.2] [sgdfc:3.5:0.3.6.0:3.8.0:9.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG433	36351637_f2_1	4331	18434	318	106	YDL017W	103	8.0(10)-5	Saccharomyces cerevisiae	[ui:ydr1017w] [pn:protein kinase:cell division control protein 7] [gn:cdc7.oaf2.d2855] [gtcf:8.5:9.4:10.1:10.2:10.8:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4:13.2] [sgdgc:3.5:0.3:6.0:3.8:0.9:5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2631	29495912_c1_5	4332	18435	1173	391	YDR122W	1051	2.5(10)-106	Saccharomyces cerevisiae	[ui:ydr122w] [pn:ser/thr protein kinase:protein kinase] [gn:kin1] [gtcf:8.5:9.4:11.1:12.13] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdgc:9.1:0:15.0.0] [db:gtc-saccharomyces cerevisiae]
b3x13461.x	16064567_f2_2	4333	18436	612	204	YDR122W	92	0.069	Saccharomyces cerevisiae	[ui:ydr122w] [pn:ser/thr protein kinase:protein kinase] [gn:kin1] [gtcf:8.5:9.4:11.1:12.13] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdgc:9.1:0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2765	6852175_f3_2	4334	18437	1233	411	YDR283C	286	6.0(10)-48	Saccharomyces cerevisiae	[ui:ydr283c] [pn:ser/thr protein kinase:protein kinase gcn2] [gn:gcn2.aas1] [gtcf:8.5:9.4:10.7:12.13] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdgc:3.0:9.2:0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3593	19532525_c3_4	4335	18438	1053	351	YDR283C	400	9.6(10)-58	Saccharomyces cerevisiae	[ui:ydr283c] [pn:ser/thr protein kinase:protein kinase gcn2] [gn:gcn2.aas1] [gtcf:8.5:9.4:10.7:12.13] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdgc:3.0:9.2:0:15.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4328	4797160_f1_1	4336	18439	792	264	YDR283C	160	2.8(10)-10	Saccharomyces cerevisiae	[ui:ydr283c] [pn:ser/thr protein kinase:protein kinase gen2] [gn:gen2:aas1] [gtcf:8.5:9.4:10.7:12.13] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:5.3:0.9:2.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG443	2384652_c3_1	4337	18440	645	215	YDR283C	334	8.6(10)-29	Saccharomyces cerevisiae	[ui:ydr283c] [pn:ser/thr protein kinase:protein kinase gen2] [gn:gen2:aas1] [gtcf:8.5:9.4:10.7:12.13] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:5.3:0.9:2.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2526	4492135_f1_1	4338	18441	1254	418	YDR477W	1345	1.8(10)-137	Saccharomyces cerevisiae	[ui:ydr477w] [pn:carbon catabolite derepressing ser/thr protein kinase:carbon catabolite derepressing protein kinase] [gn:snf1:cat1:ccr1:pas14:glc2:d8035] [gtcf:8.5:9.4:12.13:13.2] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:1.5:2:9.2:0:11]
CONTIG369	11813561_f2_1	4339	18442	438	146	YDR477W	500	6.2(10)-48	Saccharomyces cerevisiae	[ui:ydr477w] [pn:carbon catabolite derepressing ser/thr protein kinase:carbon catabolite derepressing protein kinase] [gn:snf1:cat1:ccr1:pas14:glc2:d8035] [gtcf:8.5:9.4:12.13:13.2] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:1.5:2:9.2:0:11]

CONTIG5005	820385_f3_3	4340	18443	1293	431	YDR523C	311	1.3(10)-27	Saccharomyces cerevisiae	[ui:ydr523c] [pn:ser/thr protein kinase:sporulation-specific protein 1] [gn:spsl:d9719] [gtcf:8.5:9.4:12.13:12.15:12.8] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:3.4:0:3.5:0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5636	35164093_f3_4	4341	18444	1095	365	YDR523C	237	4.2(10)-34	Saccharomyces cerevisiae	[ui:ydr523c] [pn:ser/thr protein kinase:sporulation-specific protein 1] [gn:spsl:d9719] [gtcf:8.5:9.4:12.13:12.15:12.8] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:3.4:0:3.5:0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1559	24707588_c2_5	4342	18445	903	301	YER123W	95	0.05099	Saccharomyces cerevisiae	[ui:yer123w] [pn:casein kinase, isoform 3:casein kinase i homolog 3] [gn:yek3:cki3] [gtcf:8.5:9.4:11.1:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:3.8:0:9.1:0:9.2:0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2252	20133502_c3_2	4343	18446	912	304	YER129W	448	3.2(10)-41	Saccharomyces cerevisiae	[ui:yer129w] [pn:protein kinase:serine/threonine-protein kinase pak1] [gn:pak1:sygp-orf45] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:15.0:0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5646	23648375_c2_16	4344	18447	4278	1426	YER129W	575	1.1(10)-91	Saccharomyces cerevisiae	[ui:yer129w] [pn:protein kinase:serine/threonine-protein kinase pak1] [gn:pak1:sygp-orf45] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:15.0:0:13.0.0] [db:gtc-saccharomyces cerevisiae]

b3x13076.x	24820337_c1_1	4345	18448	288	96	YER129W	127	6.0(10)-7	Saccharomyces cerevisiae	[ui:yer129w] [pn:protein kinase:serine/threonine-protein kinase pak1] [gn:pak1:sygp-orf45] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:15.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2770	35829017_c2_2	4346	18449	909	303	YFL033C	550	9.5(10)-52	Saccharomyces cerevisiae	[ui:yfl033c] [pn:similarity to s.pombe cek1 serine/threonine protein kinase:probable serine/threonine-protein kinase yfl033c] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:15.0:13.0.0] [db:gtc-saccharomyces cerevis]
CONTIG4635	14178450_f3_6	4347	18450	858	286	YFL033C	97	0.17	Saccharomyces cerevisiae	[ui:yfl033c] [pn:similarity to s.pombe cek1 serine/threonine protein kinase:probable serine/threonine-protein kinase yfl033c] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:15.0:13.0.0] [db:gtc-saccharomyces cerevis]
CONTIG4951	196890_f2_3	4348	18451	1158	386	YFL033C	290	3.5(10)-33	Saccharomyces cerevisiae	[ui:yfl033c] [pn:similarity to s.pombe cek1 serine/threonine protein kinase:probable serine/threonine-protein kinase yfl033c] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:15.0:13.0.0] [db:gtc-saccharomyces cerevis]

CONTIG4951	4164136_f2_4	4349	18452	732	244	YFL033C	179	2.8(10)-12	Saccharomyces cerevisiae	[ui:yfl033c] [pn:similarity to s.pombe cek1 serine/threonine protein kinase:probable serine/threonine-protein kinase yfl033c] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevis]
CONTIG879	1464010_c1_2	4350	18453	570	190	YFL033C	92	0.01	Saccharomyces cerevisiae	[ui:yfl033c] [pn:similarity to s.pombe cek1 serine/threonine protein kinase:probable serine/threonine-protein kinase yfl033c] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevis]
CONTIG2080	20114042_fl_2	4351	18454	1038	346	YFL029C	239	5.2(10)-19	Saccharomyces cerevisiae	[ui:yfl029c] [pn:cdk-activating protein kinase:serine/threonine-protein kinase cak1:cdk-activating kinase] [gn:cak1:civ1] [gtcf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4:13.3] [sgdfc:3.8.0:15.0.0] [db:gtc-saccharomyces cerevis]
CONTIG3639	25398512_c1_4	4352	18455	786	262	YGL180W	187	1.6(10)-17	Saccharomyces cerevisiae	[ui:ygl180w] [pn:weak similarity to ser/thr protein kinases:probable serine/threonine-protein kinase ygl180w] [gn:g1615] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5646	2191277_c3_20	4353	18456	1233	411	YGL180W	874	1.3(10)-87	Saccharomyces cerevisiae	[ui:ygl180w] [pn:weak similarity to ser/thr protein kinases:probable serine/threonine-protein kinase ygl180w] [gn:g1615] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0:0:13.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG607	9814063_f2_1	4354	18457	792	264	YGR092W	352	8.4(10)-32	Saccharomyces cerevisiae	[ui:ygr092w] [pn:ser/thr protein kinase related to dbf20p:cell cycle protein kinase] [gn:dbf2] [gtcf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4:13.3] [sgdfc:3.8.0:15.0:0] [db:gtc-saccharomyces cerevisiae]
b3x16309.x	23437827_c2_3	4355	18458	879	293	YGR092W	509	5.5(10)-59	Saccharomyces cerevisiae	[ui:ygr092w] [pn:ser/thr protein kinase related to dbf20p:cell cycle protein kinase] [gn:dbf2] [gtcf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4:13.3] [sgdfc:3.8.0:15.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3029	13835130_c1_4	4356	18459	1443	481	YGR188C	661	2.0(10)-64	Saccharomyces cerevisiae	[ui:ygr188c] [pn:ser/thr protein kinase:checkpoint serine/threonine-protein kinase bub1] [gn:bub1:g7542] [gtcf:8.5:9.4:10.1:10.2:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:3.8.0:9.5.0:15.0:0] [db:gtc-saccharomyces cerevisiae]

b1x17652.y	16287538_f3_1	4357	18460	807	269	YGR188C	194	8.5(10)-17	Saccharomyces cerevisiae	[ui:ygr188c] [pn:ser/thr protein kinase:checkpoint serine/threonine-protein kinase bub1] [gn:bub1:g7542] [gtcf:8.5:9.4:10.1:10.2:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:3.8.0:9.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4932	15745328_f2_3	4358	18461	1233	411	YHL007C	1209	4.5(10)-123	Saccharomyces cerevisiae	[ui:yhl007c] [pn:ser/thr protein kinase of the pheromone pathway:serine/threonine-protein kinase] [gn:ste20] [gtcf:8.5:9.4:12.13:12.8:12.9] [ec:2.7.1.-] [keggf:8.5:9.4:13.1:13.3] [sgdf:3.2.0:3.3.0:9.2.0:10.1.4:15.0.0] [db:gtc-sacch
CONTIG5773	24413287_c3_31	4359	18462	1623	541	YHR030C	1348	8.5(10)-138	Saccharomyces cerevisiae	[ui:yhr030c] [pn:ser/thr protein kinase of map kinase family:mitogen-activated protein kinase slit2/mpk1:map kinase mpk1] [gn:slt2:mpk1] [gtcf:8.5:9.4:12.11:12.13:12.8:13.2] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:3.1.0:3.2.0:3.8.0:10.2.
CONTIG2779	181557_c2_3	4360	18463	1161	387	YHR079C	445	6.2(10)-41	Saccharomyces cerevisiae	[ui:yhr079c] [pn:protein kinase:probable protein kinase irel precursor] [gn:irel:erm1] [gtcf:8.5:9.4:12.13:12.16:13.2] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:9.4.0:11.1.0:15.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG652	4772567_f2_1	4361	18464	804	268	YHR079C	643	3.1(10)-62	Saccharomyces cerevisiae	[ui:yhr079c] [pn:protein kinase:probable protein kinase ire1 precursor] [gn:ire1:eml] [gicf:8.5:9.4:12.13:16:13.2] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:9.4:0:11.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
b2x14728.x	11173962_f2_1	4362	18465	528	176	YHR079C	385	1.7(10)-34	Saccharomyces cerevisiae	[ui:yhr079c] [pn:protein kinase:probable protein kinase ire1 precursor] [gn:ire1:eml] [gicf:8.5:9.4:12.13:16:13.2] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:9.4:0:11.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4004	15829380_c2_7	4363	18466	1914	638	YHR082C	301	1.3(10)-25	Saccharomyces cerevisiae	[ui:yhr082c] [pn:ser/thr protein kinase:serine/threonine-protein kinase] [gn:ksp1] [gicf:8.5:9.4:10.1:10.2:12.13] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:9.5:0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4754	787550_f1_6	4364	18467	315	105	YHR082C	133	1.2(10)-7	Saccharomyces cerevisiae	[ui:yhr082c] [pn:ser/thr protein kinase:serine/threonine-protein kinase] [gn:ksp1] [gicf:8.5:9.4:10.1:10.2:12.13] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:9.5:0:15.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4227	10985682_c3_8	4365	18468	2061	687	YHR102W	1093	9.0(10)-111	Saccharomyces cerevisiae	[ui:yhr102w] [pn:ser/thr protein kinase that interacts with cdc3] p:serine/threonine-protein kinase:n-rich kinase 1] [gn:nrk1] [gicf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:3.8:0:15.0.0] [db:gic-saccharomyces cerevisi
CONTIG5005	1175001_f3_2	4366	18469	396	132	YHR102W	197	1.8(10)-14	Saccharomyces cerevisiae	[ui:yhr102w] [pn:ser/thr protein kinase that interacts with cdc3] p:serine/threonine-protein kinase:n-rich kinase 1] [gn:nrk1] [gicf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:3.8:0:15.0.0] [db:gic-saccharomyces cerevisi
CONTIG5332	31652083_f2_3	4367	18470	570	190	YHR102W	109	4.7(10)-5	Saccharomyces cerevisiae	[ui:yhr102w] [pn:ser/thr protein kinase that interacts with cdc3] p:serine/threonine-protein kinase:n-rich kinase 1] [gn:nrk1] [gicf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:3.8:0:15.0.0] [db:gic-saccharomyces cerevisi
CONTIG3439	23869215_c3_8	4368	18471	1833	611	YIL187C	566	2.2(10)-69	Saccharomyces cerevisiae	[ui:yil187c] [pn:ser/tyr dual-specificity protein kinase:mitosis inhibitor protein kinase swel] [gn:swel;j0406] [gicf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4:13.3] [sgdfc:3.8:0:15.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG3751	21681527_f3_1	4369	18472	1791	597	YJL141C	517	3.1(10)-49	Saccharomyces cerevisiae	[lui:yjl141c] [pn:ser/thr protein kinase:protein kinase yak1] [gn:yak1:j0652] [gtcf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:3.8.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3091	97531_f1_1	4370	18473	1455	485	YJL141C	1074	9.1(10)-109	Saccharomyces cerevisiae	[lui:yjl141c] [pn:ser/thr protein kinase:protein kinase yak1] [gn:yak1:j0652] [gtcf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:3.8.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3112	12695187_f3_2	4371	18474	996	332	YJL128C	562	1.7(10)-54	Saccharomyces cerevisiae	[lui:yjl128c] [pn:tyrosine protein kinase of the map kinase kinase family:polymyxin b resistance protein kinase] [gn:pbs2:hog4:sfs4:ssk4:j0699] [gtcf:8.5:9.4:12.11:12.13:13.2] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:1.5.2:10.3:11.1.0:1]
CONTIG5493	7267961_f3_7	4372	18475	1581	527	YJL106W	933	8.0(10)-94	Saccharomyces cerevisiae	[lui:yjl106w] [pn:ser/thr protein kinase:meiosis induction protein kinase smel/ime2] [gn:smel:ime2:j0817] [gtcf:8.5:9.4:12.13:12.15:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:3.4.0:3.5.0:3.8.0:15.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4749	4881586_c2_9	4373	18476	1860	620	YJL057C	337	9.8(10)-28	Saccharomyces cerevisiae	[ui:yj057c] [pn:weak similarity to human p1/eif-2a protein kinase:probable serine/threonine-protein kinase yj057c] [gn:j143] [gicf:8.5:9.4:14.3] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:13.0.0] [db:gic-saccharomyces cerevisiae]
b2x11515.x	43754438_f3_3	4374	18477	561	187	YJL006C	147	5.7(10)-10	Saccharomyces cerevisiae	[ui:yj006c] [pn:carboxy-terminal domain:ctd kinase, beta subunit:ctd kinase beta subunit:ctd kinase 38 kd subunit:ctdk-i beta subunit] [gn:ctk2:j1390] [gicf:8.5:9.4:10.1:10.2] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:4.8.2:9.5.0] [db:gt]
CONTIG3458	22071000_c3_12	4375	18478	801	267	YJR059W	401	1.6(10)-36	Saccharomyces cerevisiae	[ui:yjr059w] [pn:involved in polyamine uptake:probable serine/threonine-protein kinase yjr059w] [gn:ptk2:j1725] [gicf:8.5:9.4:12.13:12.16] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:8.0:15.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG3458	31899812_c1_5	4376	18479	978	326	YJR059W	469	6.5(10)-44	Saccharomyces cerevisiae	[ui:yjr059w] [pn:involved in polyamine uptake:probable serine/threonine-protein kinase yjr059w] [gn:ptk2:j1725] [gicf:8.5:9.4:12.13:12.16] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:8.0:15.0.0] [db:gic-saccharomyces cerevisiae]

CONTIG2622	26048442_f3_2	4377	18480	1986	662	YKL171W	235	1.8(10)-29	Saccharomyces cerevisiae	[ui:ykl171w] [pn:ser/thr protein kinase:probable serine/threonine-protein kinase ykl171w] [gn:ykl635] [gtcf:12.13:8.5:9.4] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3900	24039316_f3_4	4378	18481	1680	560	YKL139W	874	1.3(10)-87	Saccharomyces cerevisiae	[ui:ykl139w] [pn:carboxy-terminal domain:ctd kinase, alpha subunit:ctd kinase alpha subunit:ctd kinase 58 kd subunit:ctdk-i alpha subunit] [gn:ctk1] [gtcf:8.5:9.4:10.1:10.2:12.13] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:4.8.2:9.5.0:15.0]
CONTIG3582	24005340_c3_5	4379	18482	1413	471	YKL126W	1386	8.0(10)-142	Saccharomyces cerevisiae	[ui:ykl126w] [pn:ser/thr-specific protein kinase:serine/threonine-protein kinase] [gn:ypk1] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4716	15120377_f3_7	4380	18483	1476	492	YKL116C	139	2.0(10)-6	Saccharomyces cerevisiae	[ui:ykl116c] [pn:ser/thr protein kinase with similarity to rat snf1, celegans unc-51, dun1p:probable serine/threonine-protein kinase ykl116c] [gn:ykl516] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:15.0.0:13.0.0] [

CONTIG5282	33222062_f1_1	4381	18484	1320	440	YKL101W	112	0.0077	Saccharomyces cerevisiae	[ui:ykl101w] [pn:ser/thr protein kinase that interacts genetically with histone mutations:probable serine/threonine-protein kinase ykl101w] [gn:hsl:ykl453] [gtcf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4:13.3] [sgdfc:3.8.0:15]
CONTIG5594	4885787_f3_7	4382	18485	1164	388	YKL101W	438	6.4(10)-40	Saccharomyces cerevisiae	[ui:ykl101w] [pn:ser/thr protein kinase that interacts genetically with histone mutations:probable serine/threonine-protein kinase ykl101w] [gn:hsl:ykl453] [gtcf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4:13.3] [sgdfc:3.8.0:15]
b2x12381.y	14540930_f3_1	4383	18486	351	117	YKL101W	198	2.2(10)-14	Saccharomyces cerevisiae	[ui:ykl101w] [pn:ser/thr protein kinase that interacts genetically with histone mutations:probable serine/threonine-protein kinase ykl101w] [gn:hsl:ykl453] [gtcf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4:13.3] [sgdfc:3.8.0:15]
CONTIG3954	4393910_c2_4	4384	18487	996	332	YLL019C	117	0.00027	Saccharomyces cerevisiae	[ui:yll019c] [pn:ser/thr protein kinase:probable serine/threonine-protein kinase] [gn:kns1] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:15.0:0:13.0:0] [db:gtc-saccharomyces cerevisiae]

b9x13q33.x	21766543_f1_1	4385	18488	621	207	YLL019C	499	1.3(10)-47	Saccharomyces cerevisiae	[ui:yll019c] [pn:ser/thr protein kinase:probable serine/threonine-protein kinase] [gn:kns1] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:15.0:13.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG2037	13869203_f1_1	4386	18489	708	236	YLR096W	270	3.3(10)-22	Saccharomyces cerevisiae	[ui:ylr096w] [pn:ser/thr protein kinase:protein kinase] [gn:kin2] [gtcf:8.5:9.4:11.1:12.13] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:9.1:0:15.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG2037	12617180_f1_2	4387	18490	555	185	YLR096W	167	3.2(10)-11	Saccharomyces cerevisiae	[ui:ylr096w] [pn:ser/thr protein kinase:protein kinase] [gn:kin2] [gtcf:8.5:9.4:11.1:12.13] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:9.1:0:15.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3656	195437_f1_3	4388	18491	240	80	YLR113W	253	2.5(10)-21	Saccharomyces cerevisiae	[ui:ylr113w] [pn:ser/thr protein kinase of map kinase:mapk family:mitogen-activated protein kinase hog1:map kinase hog:osmosensing protein hog1] [gn:hog1:ssk3:l9354] [gtcf:8.5:9.4:12.11:12.13:13.2] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf
b9x12d90.y	11737841_f2_1	4389	18492	666	222	YLR113W	826	1.8(10)-82	Saccharomyces cerevisiae	[ui:ylr113w] [pn:ser/thr protein kinase of map kinase:mapk family:mitogen-activated protein kinase hog1:map kinase hog:osmosensing protein hog1] [gn:hog1:ssk3:l9354] [gtcf:8.5:9.4:12.11:12.13:13.2] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf

CONTIG3789	24495715_f2_1	4390	18493	1182	394	YLR248W	325	1.3(10)-55	Saccharomyces cerevisiae	[ui:ylr248w] [pn:ca/calmodulin-dependent ser/thr protein kinase:serine/threonine-protein kinase rck2:cam kinase-like protein kinase clk1] [gn:rck2:clk1:cmk3:19672] [gtcf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:3.8.0:]
CONTIG4245	203175_c2_14	4391	18494	1803	601	YLR248W	892	3.5(10)-94	Saccharomyces cerevisiae	[ui:ylr248w] [pn:ca/calmodulin-dependent ser/thr protein kinase:serine/threonine-protein kinase rck2:cam kinase-like protein kinase clk1] [gn:rck2:clk1:cmk3:19672] [gtcf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:3.8.0:]
CONTIG4407	787812_c2_6	4392	18495	1791	597	YLR362W	759	2.2(10)-109	Saccharomyces cerevisiae	[ui:ylr362w] [pn:ser/thr protein kinase of the mekk family:serine/threonine-protein kinase ste11] [gn:ste11:18039] [gtcf:8.5:9.4:12.13:12.8:12.9] [ec:2.7.1.-] [keggf:8.5:9.4:13.1] [sgdfc:3.2.0:3.3.0:10.1.4:10.4.6:15.0.0] [db:gtc-sac
CONTIG3441	25947075_c3_6	4393	18496	1005	335	YMR001C	467	9.4(10)-53	Saccharomyces cerevisiae	[ui:ymr001c] [pn:involved in regulation of dna replication:cell cycle protein kinase cdc5/msd2] [gn:cdc5:pkx2:msd2:ym8270] [gtcf:8.5:9.4:10.8:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4:13.3] [sgdfc:3.6.0:3.8.0:15.0.0] [db:gtc-saccharom

CONTIG3441	31510455_c2_5	4394	18497	993	331	YMR001C	1104	6.0(10)-112	Saccharomyces cerevisiae	[ui:yml001c] [pn:involved in regulation of dna replication:cell cycle protein kinase cdc5/msd2] [gn:cdc5:pkx2:msd2:ym8270] [gicf:8.5:9.4:10.8:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4:13.3] [sgdfc:3.6:0.3:8.0:15.0.0] [db:gic-saccharom
CONTIG153	34568942_f1_1	4395	18498	228	76	YMR104C	276	3.1(10)-23	Saccharomyces cerevisiae	[ui:yml104c] [pn:ser/thr protein kinase:serine/threonine-protein kinase ypk2/ykr2] [gn:ypk2:ykr2:ym9718] [gicf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:3.8:0:15.0.0] [db:gic-saccharomyces cerevisiae]
CONTIG3595	34073402_f3_6	4396	18499	1185	395	YMR139W	1047	6.7(10)-106	Saccharomyces cerevisiae	[ui:yml139w] [pn:ser/thr protein kinase:serine/threonine-protein kinase mds1/rim11] [gn:mds1:rim11:gsk3:ym9375] [gicf:8.5:9.4:10.1:10.2:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:3.5:0.9:5.0:15.0.0] [db:gic-saccharomyces cerevi
CONTIG2534	2454007_f3_2	4397	18500	1236	412	YNL307C	944	1.2(10)-104	Saccharomyces cerevisiae	[ui:ynl307c] [pn:ser/thr/tyr protein kinase:protein kinase mck1:meiosis and centromere regulatory kinase] [gn:mck1:ypk1:n0392] [gicf:8.5:9.4:12.13:12.15:12.8] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:3.4:0.3:5.0:3.8:0:15.0.0] [db:gic-sac

CONTIG5640	1417062_f3_5	4398	18501	915	305	YNL298W	948	2.1(10)-95	Saccharomyces cerevisiae	[ui:ynl298w] [pn:ser/thr protein kinase:serine/threonine-protein kinase cla4] [gn:cla4:n0450] [gtcf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4:13.3] [sgdf:3.9.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4277	26178451_c3_5	4399	18502	192	64	YNL161W	160	1.1(10)-10	Saccharomyces cerevisiae	[ui:ynl161w] [pn:similarity to ser/thr protein kinase:probable serine/threonine-protein kinase ynl161w] [gn:n1727] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4277	24428261_c2_4	4400	18503	1251	417	YNL161W	1705	1.3(10)-175	Saccharomyces cerevisiae	[ui:ynl161w] [pn:similarity to ser/thr protein kinase:probable serine/threonine-protein kinase ynl161w] [gn:n1727] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:15.0.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2988	14572163_c2_11	4401	18504	1509	503	YNL154C	1392	1.8(10)-142	Saccharomyces cerevisiae	[ui:ynl154c] [pn:casein kinase i isoform:casein kinase i homolog 2] [gn:yck2:ckil:n1755] [gtcf:8.5:9.4:12.13:12.8:13.2] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdf:3.1.0:3.2.0:11.1.0:15.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3895	19926502_f1_1	4402	18505	1419	473	YNL154C	1282	8.4(10)-131	Saccharomyces cerevisiae	[ui:ynl154c] [pn:casein kinase i isoform:casein kinase i homolog 2] [gn:ycf2:ckil:n1755] [gtcf:8.5:9.4:12.13:12.8:13.2] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:3.1:0.3:2.0:11.1:0.15:0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4709	12922175_c2_15	4403	18506	1035	345	YNL020C	842	3.5(10)-84	Saccharomyces cerevisiae	[ui:ynl020c] [pn:strong similarity to protein kinase pak1:probable serine/threonine-protein kinase ynl020c] [gn:n2823] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0:0.13:0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG815	32814_c1_2	4404	18507	777	259	YNR047W	549	1.8(10)-52	Saccharomyces cerevisiae	[ui:ynr047w] [pn:similarity to microtubule-associated ser/thr protein kinases:probable serine/threonine-protein kinase ynr047w] [gn:n3449] [gtcf:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:15.0:0.13:0.0] [db:gtc-saccharo]
CONTIG702	11932293_c3_4	4405	18508	945	315	YOR231W	714	1.3(10)-70	Saccharomyces cerevisiae	[ui:yor231w] [pn:ser/thr protein kinase:protein kinase mkk1/ssp32] [gn:mkk1:ssp32:o5095] [gtcf:8.5:9.4:12.13:12.8:13.2] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdfc:3.1:0.3:2.0:3.8:0.10:2.5:11.1.0:15.0:0] [db:gtc-saccharomyces cerevisiae]

CONTIG3739	22861312_c3_2	4406	18509	951	317	YOR233W	220	4.4(10)-17	Saccharomyces cerevisiae	[ui:yor233w] [pn:ser/thr protein kinase:serine/threonine-protein kinase kin4] [gn:kin4:kin31:kin3:o5220] [gicfc:8.5:9.4:12.13:14.3] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdgc:15.0:0:13.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5788	20348300_c2_22	4407	18510	294	98	YOR351C	97	0.00034	Saccharomyces cerevisiae	[ui:yor351c] [pn:ser/thr protein kinase:protein kinase mek1/mre4] [gn:mek1:mre4:o6357] [gicfc:8.5:9.4:10.1:10.2:10.8:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdgc:3.5:0:3.7:0:9.5:0:15.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5788	24882806_c1_14	4408	18511	489	163	YOR351C	412	1.3(10)-38	Saccharomyces cerevisiae	[ui:yor351c] [pn:ser/thr protein kinase:protein kinase mek1/mre4] [gn:mek1:mre4:o6357] [gicfc:8.5:9.4:10.1:10.2:10.8:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdgc:3.5:0:3.7:0:9.5:0:15.0:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5788	6734387_c3_26	4409	18512	807	269	YOR351C	169	2.0(10)-10	Saccharomyces cerevisiae	[ui:yor351c] [pn:ser/thr protein kinase:protein kinase mek1/mre4] [gn:mek1:mre4:o6357] [gicfc:8.5:9.4:10.1:10.2:10.8:12.13:12.8] [ec:2.7.1.-] [keggfc:8.5:9.4] [sgdgc:3.5:0:3.7:0:9.5:0:15.0:0] [db:gtc-saccharomyces cerevisiae]

CONTIG5171	23884758_f1_1	4410	18513	1533	511	YPL209C	447	1.3(10)-69	Saccharomyces cerevisiae	[ui:ypl209c] [pn:ser/thr protein kinase:serine/threonine-protein kinase] [gn:ipl1] [gtcf:8.5:9.4:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:3.8.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2810	897706_c1_3	4411	18514	879	293	YPL204W	1096	4.2(10)-111	Saccharomyces cerevisiae	[ui:ypl204w] [pn:casein kinase i, ser/thr/tyr protein kinase:casein kinase i homolog] [gn:hrr25] [gtcf:8.5:9.4:10.10:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:3.5.0:11.2.1:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4679	4729067_f3_3	4412	18515	1539	513	YPL153C	933	1.8(10)-114	Saccharomyces cerevisiae	[ui:ypl153c] [pn:ser/thr/tyr protein kinase:protein kinase spk1:serine-protein kinase 1] [gn:spk1:sad1:rad53:mec2:p2588] [gtcf:8.5:9.4:10.1:10.10:10.2:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4:13.3] [sgdfc:3.8.0:9.5.0:11.2.1:15.0.0]
CONTIG5596	35551337_c2_15	4413	18516	450	150	YPL153C	172	6.2(10)-12	Saccharomyces cerevisiae	[ui:ypl153c] [pn:ser/thr/tyr protein kinase:protein kinase spk1:serine-protein kinase 1] [gn:spk1:sad1:rad53:mec2:p2588] [gtcf:8.5:9.4:10.1:10.10:10.2:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4:13.3] [sgdfc:3.8.0:9.5.0:11.2.1:15.0.0]

CONTIG3883	25995694_c1_1	4414	18517	1380	460	YPL042C	958	1.0(10)-111	Saccharomyces cerevisiae	[ui:ypl042c] [pn:cyclin-dependent ser/thr protein kinase:meiotic mma stability protein kinase ume5] [gn:ume5:ssn3:srb10] [gtcf:8.5:9.4:10.1:10.2:12.13:12.8] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:1.5:2.3:5.0:4.8:2.9:5.0:15.0.0] [db:gt]
CONTIG1164	15628182_c3_2	4415	18518	696	232	YPR054W	560	2.7(10)-54	Saccharomyces cerevisiae	[ui:ypr054w] [pn:sporulation-specific map kinase:sporulation-specific mitogen-activated protein kinase smk1:map kinase smk1] [gn:smk1:yp9499] [gtcf:8.5:9.4:12.15] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:3.4.0] [db:gtc-saccharomyces cere]
CONTIG3688	2915632_c3_6	4416	18519	207	69	YPR054W	149	5.4(10)-10	Saccharomyces cerevisiae	[ui:ypr054w] [pn:sporulation-specific map kinase:sporulation-specific mitogen-activated protein kinase smk1:map kinase smk1] [gn:smk1:yp9499] [gtcf:8.5:9.4:12.15] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:3.4.0] [db:gtc-saccharomyces cere]
CONTIG472	1988425_c2_2	4417	18520	771	257	YPR161C	598	2.5(10)-58	Saccharomyces cerevisiae	[ui:ypr161c] [pn:ser/thr protein kinase:serine/threonine protein kinase sgv1] [gn:sgv1:bur1:p9584] [gtcf:8.5:9.4:12.13:12.8:12.9] [ec:2.7.1.-] [keggf:8.5:9.4] [sgdfc:3.1.0:3.3.0:3.8.0:15.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5063	12929650_f3_6	4418	18521	534	178	YMR020W	208	3.7(10)-16	Saccharomyces cerevisiae	[ui:ymr020w] [pn:suppressor of fenpropimorph resistance mutation fen2:fms1 protein] [gn:fms1:ym9711] [gtcf:8.5] [keggf:14.2] [sgdf:1.6.6] [db:gtc-saccharomyces cerevisiae]
CONTIG5063	25947078_f1_2	4419	18522	969	323	YMR020W	278	1.7(10)-43	Saccharomyces cerevisiae	[ui:ymr020w] [pn:suppressor of fenpropimorph resistance mutation fen2:fms1 protein] [gn:fms1:ym9711] [gtcf:8.5] [keggf:14.2] [sgdf:1.6.6] [db:gtc-saccharomyces cerevisiae]
CONTIG2063	4818878_f3_1	4420	18523	795	265	YDR302W	101	0.00119	Saccharomyces cerevisiae	[ui:ydr302w] [pn:weak similarity to human gpi-anchor biosynthesis protein] [gtcf:8.5:10.7] [keggf:14.2] [sgdf:1.6.7] [db:gtc-saccharomyces cerevisiae]
CONTIG5769	5188452_f2_7	4421	18524	882	294	YMR079W	988	1.2(10)-99	Saccharomyces cerevisiae	[ui:ymr079w] [pn:phosphatidylinositol:pi/phosphatidylcholine:pc transfer protein:sec14 cytosolic factor:phosphatidylinositol/phosphatidylcholine transfer protein:pi/pc tp] [gn:sec14:pit1:ym9582] [gtcf:8.5:10.7:12.10] [keggf:14.2] [s]
CONTIG3457	4301301_c3_16	4422	18525	657	219	YNL264C	334	2.3(10)-30	Saccharomyces cerevisiae	[ui:ynl264c] [pn:similarity to sec14p:hypothetical 40.7 kd protein in pik1-pol2 intergenic region] [gn:n0815] [gtcf:8.5:10.7] [keggf:14.2] [sgdf:1.6.7] [db:gtc-saccharomyces cerevisiae]

CONTIG5475	10203282_f3_6	4423	18526	1137	379	YNL264C	725	8.9(10)-72	Saccharomyces cerevisiae	[ui:ynl264c] [pn:similarity to sec14p:hypothetical 40.7 kd protein in pik1-pol2 intergenic region] [gn:m0815] [gtcf:8.5:10.7] [kegg:14.2] [sgdf:1.6.7] [db:gtc-saccharomyces cerevisiae]
CONTIG632	3913312_fl_1	4424	18527	225	75	YNL264C	139	5.4(10)-9	Saccharomyces cerevisiae	[ui:ynl264c] [pn:similarity to sec14p:hypothetical 40.7 kd protein in pik1-pol2 intergenic region] [gn:m0815] [gtcf:8.5:10.7] [kegg:14.2] [sgdf:1.6.7] [db:gtc-saccharomyces cerevisiae]
CONTIG2447	35440936_cl_3	4425	18528	708	236	YDL205C	739	2.8(10)-73	Saccharomyces cerevisiae	[ui:ydl205c] [pn:porphobilinogen deaminase:pbg:hydroxymethylbilan e synthase:hmb:pre- uroporphyrinogen synthase] [gn:hem3:d1057] [gtcf:9.10:9.11] [ec:4.3.1.8] [kegg:9.10] [sgdf:1.7.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3411	191311_c2_10	4426	18529	1047	349	YDR044W	1205	1.2(10)-122	Saccharomyces cerevisiae	[ui:ydr044w] [pn:coproporphyrinogen iii oxidase:coproporphyrinogenase:cop rogen oxidase] [gn:hem13:ydl5112] [gtcf:9.10:9.11] [ec:1.3.3.3] [kegg:9.10] [sgdf:1.7.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3839	2556288_fl_1	4427	18530	1059	353	YDR047W	1277	2.7(10)-130	Saccharomyces cerevisiae	[ui:ydr047w] [pn:uroporphyrinogen decarboxylase:upd] [gn:hem12:hem6:pop3:ydl9609] [gtcf:9.10:9.11] [ec:4.1.1.37] [kegg:9.10] [sgdf:1.7.1:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3082	10995167_c3_11	4428	18531	744	248	YGL040C	793	5.5(10)-79	Saccharomyces cerevisiae	[ui:ygl040c] [pn:delta-aminolevulinic acid dehydratase:porphobilinogen synthase:aladh] [gn:hem2] [gtcf:9.10:9.11] [ec:4.2.1.24] [keggfc:9.10] [sgdfc:1.7.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3082	36351513_c2_7	4429	18532	513	171	YGL040C	469	1.2(10)-44	Saccharomyces cerevisiae	[ui:ygl040c] [pn:delta-aminolevulinic acid dehydratase:porphobilinogen synthase:aladh] [gn:hem2] [gtcf:9.10:9.11] [ec:4.2.1.24] [keggfc:9.10] [sgdfc:1.7.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5819	163930_c1_35	4430	18533	1839	613	YKR069W	814	1.3(10)-111	Saccharomyces cerevisiae	[ui:ykr069w] [pn:siroheme synthase:probable uroporphyrin-iii c-methyltransferase:urogen iii methylase:sumt:uroporphyrinogen iii methylase:urom] [gn:met1] [gtcf:9.10:9.11] [ec:2.1.1.107] [keggfc:9.10] [sgdfc:1.7.1] [db:gtc-saccharomyc]
CONTIG5455	22344025_c1_7	4431	18534	630	210	YOR278W	364	1.6(10)-33	Saccharomyces cerevisiae	[ui:yor278w] [pn:uroporphyrinogen iii synthase:uroporphyrinogen-iii synthase:urosinthase:uroporphyrinogen-iii cosynthetase:hydroxymethylbilane hydrolyase:cyclizing:uroiis] [gn:hem4:orf1:o5463] [gtcf:9.10:9.11] [ec:4.2.1.75] [keggfc:9.10] [

CONTIG5706	13673313_c2_21	4432	18535	1092	364	YBL033C	619	1.5(10)-60	Saccharomyces cerevisiae	[ui:ybr033c] [pn:gnp cyclohydrolase ii] [gn:rib1:ybr0417] [gtcf:9.10:9.11:9.2] [ec:3.5.4.25] [keggfc:9.2] [sgdgc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5647	14238805_c2_19	4433	18536	882	294	YBR035C	648	1.3(10)-63	Saccharomyces cerevisiae	[ui:ybr035c] [pn:pyridoxamine-phosphate oxidase:pyridoxamine 5"-phosphate oxidase:pnp/pmp oxidase] [gn:pdx3:ybr0321] [gtcf:9.10:9.11:9.3] [ec:1.4.3.5] [keggfc:9.3] [sgdgc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG835	31673958_f2_1	4434	18537	771	257	YBR035C	696	1.1(10)-68	Saccharomyces cerevisiae	[ui:ybr035c] [pn:pyridoxamine-phosphate oxidase:pyridoxamine 5"-phosphate oxidase:pnp/pmp oxidase] [gn:pdx3:ybr0321] [gtcf:9.10:9.11:9.3] [ec:1.4.3.5] [keggfc:9.3] [sgdgc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3539	869037_f1_2	4435	18538	309	103	YBR153W	238	3.6(10)-20	Saccharomyces cerevisiae	[ui:ybr153w] [pn:htp reductase] [gn:rib7:ybr1203] [gtcf:9.10:9.11] [keggfc:14.2] [sgdgc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4859	4973762_f2_4	4436	18539	279	93	YBR176W	163	8.6(10)-12	Saccharomyces cerevisiae	[ui:ybr176w] [pn:strong similarity to e.coli 3-methyl-2-oxobutanoate hydroxymethyltransferase:putative 3-methyl-2-oxobutanoate hydroxymethyltransferase:ketopantoate hydroxymethyltransferase] [gn:ybr1238] [gtcf:9.10:9.11:9.5:9.6] [ec:

CONTIG5523	2003502_c1_16	4437	18540	855	285	YBR256C	701	3.1(10)-69	Saccharomyces cerevisiae	[ui:ybr256c] [pn:riboflavin synthase, alpha chain:riboflavin synthase alpha chain] [gn:rib5:ybr1724] [gtcf:9.10:9.11:9.2] [ec:2.5.1.9] [keggf:9.2] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4978	23486660_c2_10	4438	18541	657	219	YDL045C	363	2.0(10)-33	Saccharomyces cerevisiae	[ui:ydl045c] [pn:flavin adenine dinucleotide:fad synthetase:fmn adenyltransferase:fad pyrophosphorylase:flavin adenine dinucleotide synthetase] [gn:fad1:d2702] [gtcf:9.10:9.11:9.2] [ec:2.7.7.2] [keggf:9.2] [sgdf:1.7.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5735	485306_c1_14	4439	18542	360	120	YDR487C	296	2.6(10)-26	Saccharomyces cerevisiae	[ui:ydr487c] [pn:3,4-dihydroxy-2-butanone 4-phosphate synthase] [gn:rib3] [gtcf:9.10:9.11] [keggf:14.2] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5120	3945937_c1_4	4440	18543	912	304	YFR047C	1008	9.0(10)-102	Saccharomyces cerevisiae	[ui:yfr047c] [pn:similarity to human quinolinate phosphoribosyltransferase:putative nicotinate-nucleotide pyrophosphorylase:carboxylating:quinolinate phosphoribosyltransferase:decarboxylating:qaprtase] [gtcf:9.10:9.11:9.4] [ec:2.4.2.

CONTIG5490	6140937_c1_9	4441	18544	1407	469	YGL125W	1322	4.7(10)-135	Saccharomyces cerevisiae	[ui:ygl125w] [pn:similarity to human methylenetetrahydrofolate reductase:hypothetical 68.5 kd protein in scs3-sup44 intergenic region] [gn:g2882] [gtcf:10.7] [keggf:14.2] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5728	15675637_c2_20	4442	18545	1524	508	YGR255C	792	7.0(10)-79	Saccharomyces cerevisiae	[ui:ygr255c] [pn:similarity to e.coli ubh and visc proteins:hypothetical 53.5 kd protein in eno1-gnd2 intergenic region] [gn:g9165] [gtcf:9.10:9.11] [keggf:14.2] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5513	24004557_f3_9	4443	18546	330	110	YGR267C	117	6.0(10)-7	Saccharomyces cerevisiae	[ui:ygr267c] [pn:gtp cyclohydrolase i:gtp-ch-i] [gn:fol2:g9349] [gtcf:9.10:9.11:9.6] [ec:3.5.4.16] [keggf:9.7] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5637	1070376_c3_25	4444	18547	498	166	YGR267C	653	3.7(10)-64	Saccharomyces cerevisiae	[ui:ygr267c] [pn:gtp cyclohydrolase i:gtp-ch-i] [gn:fol2:g9349] [gtcf:9.10:9.11:9.6] [ec:3.5.4.16] [keggf:9.7] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5560	4415700_f3_6	4445	18548	1263	421	YGR286C	1193	2.2(10)-121	Saccharomyces cerevisiae	[ui:ygr286c] [pn:biotin synthetase] [gn:bio2] [gtcf:9.10:9.11:9.6] [ec:2.8.1.-] [keggf:9.6] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5546	24275077_c2_17	4446	18549	372	124	YHR042W	300	8.1(10)-26	Saccharomyces cerevisiae	[ui:yhr042w] [pn:nadph-cytochrome p450 reductase:cpr] [gn:ncpl:ncpr1:prd1] [gtcf:9.10:9.11:9.13:12.12:12.16] [ec:1.6.2.4] [keggf:9.12] [sgdf:1.7.1:9.4.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5546	25782638_c1_14	4447	18550	1713	571	YHR042W	1229	3.5(10)-125	Saccharomyces cerevisiae	[ui:yhr042w] [pn:nadph-cytochrome p450 reductase:cpr] [gn:ncpl:ncpr1:prd1] [gtcf:9.10:9.11:9.13:12.12:12.16] [ec:1.6.2.4] [keggf:9.12] [sgdf:1.7.1:9.4.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3135	36057828_f3_3	4448	18551	609	203	YHR111W	435	4.7(10)-41	Saccharomyces cerevisiae	[ui:yhr111w] [pn:similarity to molybdopter biosynthesis proteins:hypothetical 49.4 kd protein in cdc12-orc6 intergenic region] [gtcf:9.10:9.11] [keggf:14.2] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3468	4335825_f3_5	4449	18552	402	134	YHR111W	282	1.3(10)-24	Saccharomyces cerevisiae	[ui:yhr111w] [pn:similarity to molybdopter biosynthesis proteins:hypothetical 49.4 kd protein in cdc12-orc6 intergenic region] [gtcf:9.10:9.11] [keggf:14.2] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]

CONTIG4532	4162762_c2_8	4450	18553	255	85	YJR142W	248	3.1(10)-21	Saccharomyces cerevisiae	[ui:yjr142w] [pn:similarity to thiamin pyrophosphokinase:hypothetical 39.7 kd protein in hom6-pmt4 intergenic region] [gn:j2171] [gtcf:9.10:9.11] [keggf:14.2] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2848	29394562_f2_2	4451	18554	894	298	YKL027W	970	9.6(10)-98	Saccharomyces cerevisiae	[ui:ykl027w] [pn:similarity to e.coli molybdopterin-converting factor chlN:hypothetical 50.3 kd protein in tfal-pan3 intergenic region] [gtcf:9.10:9.11] [keggf:14.2] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2513	21964455_f3_1	4452	18555	1329	443	YMR113W	669	7.5(10)-66	Saccharomyces cerevisiae	[ui:ymr113w] [pn:similarity to folylpolyglutamate synthetases and strong similarity to hypothetical protein yk1132c] [gtcf:9.10:9.11] [keggf:14.2] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3763	27050781_c3_5	4453	18556	951	317	YNL256W	521	1.7(10)-49	Saccharomyces cerevisiae	[ui:ynl256w] [pn:similarity to bacterial dihydropteroate synthase:probable folic acid synthesis protein:contains dihydropteroate synthase:dhps:dihydropteroate pyrophosphorylase:2-amino-4-hydroxy-6-hydroxymethyl dihydropteridine pyropho

CONTIG5793	20098165_c2_23	4454	18557	1752	584	YNL256W	718	4.9(10)-71	Saccharomyces cerevisiae	[ui:ynl256w] [pn:similarity to bacterial dihydropteroate synthase:probable folic acid synthesis protein:contains:dihydropteroate synthase:dhrs:dihydropteroate pyrophosphorylase:2-amino-4-hydroxy-6-hydroxymethyl-dihydropteridine pyropho
CONTIG4540	4897188_c1_6	4455	18558	648	216	YNR057C	412	1.3(10)-38	Saccharomyces cerevisiae	[ui:ynr057c] [pn:putative dethiobiotin synthetase:dethiobiotin synthetase:dtbs] [gn:bio4:n3506] [gtcf:9.10:9.11:9.6] [ec:6.3.3.3] [keggfc:9.6] [sgdgc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3721	21881311_f2_2	4456	18559	453	151	YOL151W	317	1.5(10)-28	Saccharomyces cerevisiae	[ui:yol151w] [pn:similarity to plant dihydroflavonol-4-reductases] [gtcf:9.10:9.11] [keggfc:14.2] [sgdgc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3787	21876287_c2_6	4457	18560	1041	347	YOL151W	549	4.0(10)-53	Saccharomyces cerevisiae	[ui:yol151w] [pn:similarity to plant dihydroflavonol-4-reductases] [gtcf:9.10:9.11] [keggfc:14.2] [sgdgc:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3950	23610936_f3_2	4458	18561	804	268	YOL151W	521	3.7(10)-50	Saccharomyces cerevisiae	[ui:yol151w] [pn:similarity to plant dihydroflavonol-4-reductases] [gtcf:9.10:9.11] [keggfc:14.2] [sgdgc:1.7.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5221	24414136_f2_10	4459	18562	453	151	YOL151W	255	5.7(10)-22	Saccharomyces cerevisiae	[ui:yol151w] [pn:similarity to plant dihydroflavonol-4-reductases] [gdcf:9.10:9.11] [keggf:14.2] [sgdcf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5494	24064437_f3_7	4460	18563	189	63	YOL151W	105	2.7(10)-5	Saccharomyces cerevisiae	[ui:yol151w] [pn:similarity to plant dihydroflavonol-4-reductases] [gdcf:9.10:9.11] [keggf:14.2] [sgdcf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5568	24406555_c1_13	4461	18564	1059	353	YOL151W	806	2.2(10)-80	Saccharomyces cerevisiae	[ui:yol151w] [pn:similarity to plant dihydroflavonol-4-reductases] [gdcf:9.10:9.11] [keggf:14.2] [sgdcf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5664	26250632_c3_22	4462	18565	645	215	YOL151W	385	9.5(10)-36	Saccharomyces cerevisiae	[ui:yol151w] [pn:similarity to plant dihydroflavonol-4-reductases] [gdcf:9.10:9.11] [keggf:14.2] [sgdcf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5708	2525201_c1_18	4463	18566	633	211	YOL151W	301	7.5(10)-27	Saccharomyces cerevisiae	[ui:yol151w] [pn:similarity to plant dihydroflavonol-4-reductases] [gdcf:9.10:9.11] [keggf:14.2] [sgdcf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2992	32070305_c3_6	4464	18567	549	183	YOL143C	581	1.6(10)-56	Saccharomyces cerevisiae	[ui:yol143c] [pn:6,7-dimethyl-8-ribityllumazine synthase:dmrl synthase:lumazine synthase:riboflavin synthase beta chain] [gn:rib4] [gdcf:9.10:9.11:9.2] [ec:2.5.1.9] [keggf:9.2] [sgdcf:1.7.1] [db:gtc-saccharomyces cerevisiae]

CONTIG1475	20506952_c3_3	4465	18568	663	221	YOL066C	359	1.7(10)-32	Saccharomyces cerevisiae	[ui:yol066c] [pn:drap deaminase] [gn:rib2] [gtcf:9.10:9.11] [keggf:14.2] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2804	5892535_f3_3	4466	18569	1275	425	YOL066C	1015	1.7(10)-102	Saccharomyces cerevisiae	[ui:yol066c] [pn:drap deaminase] [gn:rib2] [gtcf:9.10:9.11] [keggf:14.2] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG873	20506952_f2_1	4467	18570	624	208	YOL066C	359	1.7(10)-32	Saccharomyces cerevisiae	[ui:yol066c] [pn:drap deaminase] [gn:rib2] [gtcf:9.10:9.11] [keggf:14.2] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5165	26440792_c1_10	4468	18571	336	112	YOL049W	298	4.0(10)-26	Saccharomyces cerevisiae	[ui:yol049w] [pn:strong similarity to s.pombe gsa1 protein] [gtcf:9.10:9.11] [keggf:14.2] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5165	11189587_c3_17	4469	18572	441	147	YOL049W	294	1.2(10)-25	Saccharomyces cerevisiae	[ui:yol049w] [pn:strong similarity to s.pombe gsa1 protein] [gtcf:9.10:9.11] [keggf:14.2] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3711	892056_f1_2	4470	18573	456	152	YOL049W	284	1.5(10)-24	Saccharomyces cerevisiae	[ui:yol049w] [pn:strong similarity to s.pombe gsa1 protein] [gtcf:9.10:9.11] [keggf:14.2] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2084	12612755_c2_5	4471	18574	717	239	YOR143C	318	1.2(10)-28	Saccharomyces cerevisiae	[ui:yor143c] [pn:thiamin pyrophosphokinase:tpk:thiamin kinase] [gn:thi80:yor373c] [gtcf:9.10:9.1:9.11] [ec:2.7.6.2] [keggf:9.1] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]

CONTIG3157	21891955_c2_5	4472	18575	300	100	YOR143C	148	4.4(10)-10	Saccharomyces cerevisiae	[ui:yor143c] [pn:thiamin pyrophosphokinase:tpk:thiamin kinase] [gn:thi80:yor3373c] [gdcf:9.10:9.1:9.11] [ec:2.7.6.2] [keggf:9.1] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2709	22550026_f1_1	4473	18576	1011	337	YOR209C	946	3.3(10)-95	Saccharomyces cerevisiae	[ui:yor209c] [pn:nicotinate phosphoribosyltransferase:probable nicotinate phosphoribosyltransferase:naptase] [gn:npt1] [gdcf:9.10:9.11:9.4] [ec:2.4.2.1] [keggf:9.4] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4348	22437775_f1_1	4474	18577	1557	519	YOR241W	1257	3.7(10)-128	Saccharomyces cerevisiae	[ui:yor241w] [pn:similarity to tetrahydrofolylpolyglutamate synthase] [gdcf:9.10:9.11] [keggf:14.2] [sgdf:1.7.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1422	119015_f3_1	4475	18578	525	175	YPL214C	390	2.7(10)-36	Saccharomyces cerevisiae	[ui:ypl214c] [pn:thiamin-phosphate pyrophosphorylase and hydroxyethylthiazole kinase:thiamin biosynthetic bifunctional enzyme:contains:thiamin-phosphate pyrophosphorylase:tmp pyrophosphorylase:tmp-ppase / hydroxyethylthiazole kinase:4

CONTIG5317	20601527_c3_15	4476	18579	1095	365	YPL023C	842	3.5(10)-84	Saccharomyces cerevisiae	[ui:ypl023c] [pn:similarity to human methylentetrahydrofolate reductase:putative methylentetrahydrofolate reductase] [gn:lpb8c] [gicfc:10.7] [ec:1.5.1.20] [keggfc:14.1] [sgdgc:1.7.1] [db:gte-saccharomyces cerevisiae]
CONTIG5798	26689001_f1_1	4477	18580	822	274	YIR008C	732	1.6(10)-72	Saccharomyces cerevisiae	[ui:yir008c] [pn:dna-directed dna polymerase alpha 48kda subunit:dna primase:dna primase small chain:p48] [gn:pril:yib8c] [gicfc:9.12:10.1:10.2:10.8] [ec:2.7.7.-] [keggfc:9.13] [sgdgc:3.6.0:9.5.0] [db:gte-saccharomyces cerevisiae]
CONTIG5798	24801275_f2_10	4478	18581	636	212	YIR008C	250	4.0(10)-21	Saccharomyces cerevisiae	[ui:yir008c] [pn:dna-directed dna polymerase alpha 48kda subunit:dna primase:dna primase small chain:p48] [gn:pril:yib8c] [gicfc:9.12:10.1:10.2:10.8] [ec:2.7.7.-] [keggfc:9.13] [sgdgc:3.6.0:9.5.0] [db:gte-saccharomyces cerevisiae]
CONTIG1903	31423252_f3_1	4479	18582	1110	370	YKL045W	756	4.5(10)-75	Saccharomyces cerevisiae	[ui:ykl045w] [pn:dna-directed dna polymerase alpha , 58 kd subunit:dna primase:dna primase large chain:p58] [gn:prl2:ykl258] [gicfc:9.12:10.1:10.2:10.8] [ec:2.7.7.-] [keggfc:9.13] [sgdgc:3.6.0:9.5.0] [db:gte-saccharomyces cerevisiae]

CONTIG4654	978541_c2_9	4480	18583	660	220	YKL045W	373	1.8(10)-34	Saccharomyces cerevisiae	[ui:ykl045w] [pn:dna-directed dna polymerase alpha , 58 kd subunit:dna primase:dna primase large chain:p58] [gn:prl2:ykl258] [gicf:9.12:10.1:10.2:10.8] [ec:2.7.7.-] [keggf:9.13] [sgdgc:3.6:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5809	32680300_c2_24	4481	18584	783	261	YOR346W	107	0.006	Saccharomyces cerevisiae	[ui:yor346w] [pn:dna repair protein:dna repair protein rev1] [gn:rev1:o6339] [gicf:9.12:10.10] [ec:2.7.7.-] [keggf:9.13] [sgdgc:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5809	2910900_c2_23	4482	18585	2583	861	YOR346W	737	4.2(10)-100	Saccharomyces cerevisiae	[ui:yor346w] [pn:dna repair protein:dna repair protein rev1] [gn:rev1:o6339] [gicf:9.12:10.10] [ec:2.7.7.-] [keggf:9.13] [sgdgc:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5342	15640660_f3_11	4483	18586	1545	515	YDL141W	712	2.1(10)-70	Saccharomyces cerevisiae	[ui:ydl141w] [pn:biotin holocarboxylase synthetase:biotin--protein ligase:biotin apo-protein ligase:biotin--] [gn:bpl1:acc2:d2140] [gicf:9.12:9.6:10.7] [keggf:9.6] [sgdgc:1.7.2:6.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5342	20901412_f2_8	4484	18587	546	182	YDL141W	295	2.7(10)-25	Saccharomyces cerevisiae	[ui:ydl141w] [pn:biotin holocarboxylase synthetase:biotin--protein ligase:biotin apo-protein ligase:biotin--] [gn:bpl1:acc2:d2140] [gtcf:9.12:9.6:10.7] [keggf:9.6] [sgdfc:1.7.2:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5148	2145453_c1_5	4485	18588	1329	443	YAR071W	935	5.0(10)-94	Saccharomyces cerevisiae	[ui:yar071w] [pn:secreted acid phosphatase:acid phosphatase precursor:p56] [gn:pho11] [gtcf:9.13:9.2:13.10] [ec:3.1.3.2] [keggf:9.2:9.12] [sgdfc:1.4.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4439	20023552_c3_10	4486	18589	1494	498	YAR071W	1016	1.3(10)-102	Saccharomyces cerevisiae	[ui:yar071w] [pn:secreted acid phosphatase:acid phosphatase precursor:p56] [gn:pho11] [gtcf:9.13:9.2:13.10] [ec:3.1.3.2] [keggf:9.2:9.12] [sgdfc:1.4.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4782	29588513_f2_2	4487	18590	1215	405	YAR071W	969	1.2(10)-97	Saccharomyces cerevisiae	[ui:yar071w] [pn:secreted acid phosphatase:acid phosphatase precursor:p56] [gn:pho11] [gtcf:9.13:9.2:13.10] [ec:3.1.3.2] [keggf:9.2:9.12] [sgdfc:1.4.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5080	23626501_c3_16	4488	18591	1065	355	YDR541C	530	4.0(10)-51	Saccharomyces cerevisiae	[ui:ydr541c] [pn:similarity to dihydroflavonol-4-reductases] [gtcf:9.13] [keggf:14.2] [sgdfc:1.7.5] [db:gtc-saccharomyces cerevisiae]

CONTIG4287	30476526_f3_7	4489	18592	543	181	YER183C	152	4.7(10)-11	Saccharomyces cerevisiae	[ui:yer183c] [pn:similarity to human 5,10-methylenetetrahydrofolate synthetase:hypothetical 24.1 kd protein in isc10.3"region] [gtcf:10.7] [keggfc:14.2] [sgdfc:1.7.5] [db:gtc-saccharomyces cerevisiae]
CONTIG2130	19062_c1_4	4490	18593	621	207	YGL157W	200	5.2(10)-25	Saccharomyces cerevisiae	[ui:ygl157w] [pn:similarity to v.vinifera dihydroflavonol 4-reductase:hypothetical 38.1 kd protein in rck1-ams1 intergenic region] [gn:g1857] [gtcf:9.13] [keggfc:14.2] [sgdfc:1.7.5] [db:gtc-saccharomyces cerevisiae]
CONTIG5595	4725438_c2_9	4491	18594	375	125	YGL157W	105	2.7(10)-5	Saccharomyces cerevisiae	[ui:ygl157w] [pn:similarity to v.vinifera dihydroflavonol 4-reductase:hypothetical 38.1 kd protein in rck1-ams1 intergenic region] [gn:g1857] [gtcf:9.13] [keggfc:14.2] [sgdfc:1.7.5] [db:gtc-saccharomyces cerevisiae]
CONTIG3659	20003802_fl_1	4492	18595	252	84	YGL157W	106	2.1(10)-5	Saccharomyces cerevisiae	[ui:ygl157w] [pn:similarity to v.vinifera dihydroflavonol 4-reductase:hypothetical 38.1 kd protein in rck1-ams1 intergenic region] [gn:g1857] [gtcf:9.13] [keggfc:14.2] [sgdfc:1.7.5] [db:gtc-saccharomyces cerevisiae]
CONTIG5521	10719657_c3_31	4493	18596	1083	361	YGR144W	781	1.0(10)-77	Saccharomyces cerevisiae	[ui:ygr144w] [pn:thiamine-repressed protein:mol1 protein] [gn:mol1:esp35:thi4:g620] [gtcf:9.13:13.2] [keggfc:14.2] [sgdfc:1.7.5:11.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1078	4885950_c3_3	4494	18597	738	246	YDR039C	873	1.8(10)-87	Saccharomyces cerevisiae	[ui:ydr039c] [pn:p-type atpase involved in na ⁺ efflux:sodium transport atpase 2] [gn:ena2:pmr2b] [gtcf:12.5:9.6] [ec:3.6.1.-] [keggfc:9.7] [sgdgc:1.8.2:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1948	15632052_fl_1	4495	18598	390	130	YDR039C	342	6.4(10)-30	Saccharomyces cerevisiae	[ui:ydr039c] [pn:p-type atpase involved in na ⁺ efflux:sodium transport atpase 2] [gn:ena2:pmr2b] [gtcf:12.5:9.6] [ec:3.6.1.-] [keggfc:9.7] [sgdgc:1.8.2:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4224	5119000_c2_5	4496	18599	927	309	YDR039C	695	6.0(10)-68	Saccharomyces cerevisiae	[ui:ydr039c] [pn:p-type atpase involved in na ⁺ efflux:sodium transport atpase 2] [gn:ena2:pmr2b] [gtcf:12.5:9.6] [ec:3.6.1.-] [keggfc:9.7] [sgdgc:1.8.2:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4224	4884385_c1_4	4497	18600	768	256	YDR039C	437	4.4(10)-40	Saccharomyces cerevisiae	[ui:ydr039c] [pn:p-type atpase involved in na ⁺ efflux:sodium transport atpase 2] [gn:ena2:pmr2b] [gtcf:12.5:9.6] [ec:3.6.1.-] [keggfc:9.7] [sgdgc:1.8.2:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5529	25680192_c2_13	4498	18601	474	158	YDR039C	365	2.2(10)-32	Saccharomyces cerevisiae	[ui:ydr039c] [pn:p-type atpase involved in na ⁺ efflux:sodium transport atpase 2] [gn:ena2:pmr2b] [gtcf:12.5:9.6] [ec:3.6.1.-] [keggfc:9.7] [sgdgc:1.8.2:7.8.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2005	16844757_f1_1	4499	18602	777	259	YEL031W	915	6.5(10)-92	Saccharomyces cerevisiae	[ui:yel031w] [pn:p-type atpase:probable cation-transporting atpase_yel031w] [gn:spf1] [gtcf:12.5:9.6] [ec:3.6.1.-] [keggfc:9.7] [sgdfe:1.8.2:7.2:7.8.0] [db:gtc- saccharomyces cerevisiae]
CONTIG3972	4117930_c3_7	4500	18603	2061	687	YEL031W	2065	8.9(10)-214	Saccharomyces cerevisiae	[ui:yel031w] [pn:p-type atpase:probable cation-transporting atpase_yel031w] [gn:spf1] [gtcf:12.5:9.6] [ec:3.6.1.-] [keggfc:9.7] [sgdfe:1.8.2:7.2:7.8.0] [db:gtc- saccharomyces cerevisiae]
CONTIG3972	10550012_c3_6	4501	18604	672	224	YEL031W	307	4.2(10)-26	Saccharomyces cerevisiae	[ui:yel031w] [pn:p-type atpase:probable cation-transporting atpase_yel031w] [gn:spf1] [gtcf:12.5:9.6] [ec:3.6.1.-] [keggfc:9.7] [sgdfe:1.8.2:7.2:7.8.0] [db:gtc- saccharomyces cerevisiae]
CONTIG4721	14270187_f3_1	4502	18605	3039	1013	YER172C	1797	2.2(10)-185	Saccharomyces cerevisiae	[ui:yer172c] [pn:rna helicase-related protein:pre-mrna splicing helicase brr2] [gn:brr2:rss1:sygp-orf66] [gtcf:9.6:10.1:10.2] [ec:3.6.1.-] [keggfc:9.7] [sgdfe:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5651	10182681_f3_13	4503	18606	1635	545	YER172C	661	8.5(10)-69	Saccharomyces cerevisiae	[ui:yer172c] [pn:rna helicase-related protein:pre-mrna splicing helicase brr2] [gn:brr2:rss1:sygp-orf66] [gtcf:9.6:10.1:10.2] [ec:3.6.1.-] [keggfc:9.7] [sgdfe:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2357	7292217_c1_4	4504	18607	1713	571	YIL048W	1688	8.0(10)-174	Saccharomyces cerevisiae	[ui:yil048w] [pn:similarity to amino-phospholipids-ATPase drs2p:probable cation-transporting ATPase yil048w] [gtcf:12.5:9.6] [ec:3.6.1.-] [keggfc:9.7] [sgdfc:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3255	6285256_f2_2	4505	18608	819	273	YIL048W	892	1.8(10)-89	Saccharomyces cerevisiae	[ui:yil048w] [pn:similarity to amino-phospholipids-ATPase drs2p:probable cation-transporting ATPase yil048w] [gtcf:12.5:9.6] [ec:3.6.1.-] [keggfc:9.7] [sgdfc:7.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1626	2909662_f2_2	4506	18609	672	224	YIL092W	331	1.1(10)-28	Saccharomyces cerevisiae	[ui:yil092w] [pn:atp-dependent dna helicase:atp-dependent dna helicase srs2] [gn:srs2:radh:hpr5:j0913] [gtcf:9.6:10.1:10.10:10.2] [ec:3.6.1.-] [keggfc:9.7] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3330	21726626_c2_3	4507	18610	1356	452	YIL092W	573	1.3(10)-54	Saccharomyces cerevisiae	[ui:yil092w] [pn:atp-dependent dna helicase:atp-dependent dna helicase srs2] [gn:srs2:radh:hpr5:j0913] [gtcf:9.6:10.1:10.10:10.2] [ec:3.6.1.-] [keggfc:9.7] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG3407	21697181_f3_3	4508	18611	3147	1049	YAL051W	157	2.7(10)-7	Saccharomyces cerevisiae	[ui:yal051w] [pn:peroxisome proliferating transcription factor:putative 118.2 kd transcriptional regulatory protein in acs1-gev3 intergenic region] [gn:oafl:fun43] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:1.6.4:4.8.2:9.5.0] [db:gtc-sacc
CONTIG4406	4116551_f2_1	4509	18612	2079	693	YAL051W	134	4.5(10)-5	Saccharomyces cerevisiae	[ui:yal051w] [pn:peroxisome proliferating transcription factor:putative 118.2 kd transcriptional regulatory protein in acs1-gev3 intergenic region] [gn:oafl:fun43] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:1.6.4:4.8.2:9.5.0] [db:gtc-sacc
CONTIG5212	488430_f3_11	4510	18613	735	245	YAL025C	675	1.8(10)-66	Saccharomyces cerevisiae	[ui:yal025c] [pn:nuclear viral propagation protein:protein] [gn:mak16] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdf:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1717	35439526_f2_2	4511	18614	1155	385	YAL021C	909	2.7(10)-91	Saccharomyces cerevisiae	[ui:yal021c] [pn:transcriptional regulator:glucose-repressible alcohol dehydrogenase catabolite repressor protein 4] [gn:ccr4:fun27] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:4.8.2:9.5.0] [db:gtc-saccharom

CONTIG620	9848317_f3_3	4512	18615	384	128	YAL021C	398	3.5(10)-36	Saccharomyces cerevisiae	[ui:yal021c] [pn:transcriptional regulator:glucose-repressible alcohol dehydrogenase transcriptional effector:carbon catabolite repressor protein 4] [gn:ccr4:fun27] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8.2-9.5.0] [db:gtc-saccharom]
CONTIG3958	164002_f3_5	4513	18616	390	130	YAL019W	364	3.0(10)-32	Saccharomyces cerevisiae	[ui:yal019w] [pn:similarity to helicases of the snf2/rad54 family:hypothetical 128.5 kd helicase in atsl-tpd3 intergenic region] [gn:yal001:fun30] [gicfc:10.1:10.10:10.2] [keggfc:14.2] [sgdgc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevi]
CONTIG4665	117805_c1_10	4514	18617	1326	442	YAL019W	94	0.41999	Saccharomyces cerevisiae	[ui:yal019w] [pn:similarity to helicases of the snf2/rad54 family:hypothetical 128.5 kd helicase in atsl-tpd3 intergenic region] [gn:yal001:fun30] [gicfc:10.1:10.10:10.2] [keggfc:14.2] [sgdgc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevi]
CONTIG676	986561_f3_1	4515	18618	1038	346	YAL019W	945	4.2(10)-95	Saccharomyces cerevisiae	[ui:yal019w] [pn:similarity to helicases of the snf2/rad54 family:hypothetical 128.5 kd helicase in atsl-tpd3 intergenic region] [gn:yal001:fun30] [gicfc:10.1:10.10:10.2] [keggfc:14.2] [sgdgc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevi]

b3x12445.y	10757692_c3_3	4516	18619	270	90	YAL019W	93	0.0025	Saccharomyces cerevisiae	[ui:yal019w] [pn:similarity to helicases of the snf2/rad54 family:hypothetical 128.5 kd helicase in ats1-tpd3 intergenic region] [gn:yal001:fun30] [gtcfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevi
CONTIG5393	24392825_c1_17	4517	18620	2040	680	YAL001C	316	1.7(10)-26	Saccharomyces cerevisiae	[ui:yal001c] [pn:tfiiic:transcription initiation factor subunit, 138 kd:transcription factor tau 138 kd subunit:tfiiic 138 kd subunit] [gn:tfc3:tsv115:fun24] [gtcfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.1.0:4.4.0:9.5.0] [db:gtc- sacch
CONTIG5393	10657757_c3_19	4518	18621	2232	744	YAL001C	126	3.5(10)-16	Saccharomyces cerevisiae	[ui:yal001c] [pn:tfiiic:transcription initiation factor subunit, 138 kd:transcription factor tau 138 kd subunit:tfiiic 138 kd subunit] [gn:tfc3:tsv115:fun24] [gtcfc:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.1.0:4.4.0:9.5.0] [db:gtc- sacch

CONTIG5814	29491427_f2_13	4519	18622	1098	366	YAR007C	788	1.8(10)-78	Saccharomyces cerevisiae	[ui:yar007c] [pn:dna replication factor a, 69 kd subunit:replication factor-a protein 1:rf-a:single-stranded dna-binding protein:dna binding protein buf2] [gn:rfal:buf2:rpal:fun3] [gtcf:10.1:10.2:10.8:12.9] [keggfc:14.2] [sgdfc:3.3.0]
CONTIG5814	4806312_f3_26	4520	18623	303	101	YAR007C	139	1.3(10)-8	Saccharomyces cerevisiae	[ui:yar007c] [pn:dna replication factor a, 69 kd subunit:replication factor-a protein 1:rf-a:single-stranded dna-binding protein:dna binding protein buf2] [gn:rfal:buf2:rpal:fun3] [gtcf:10.1:10.2:10.8:12.9] [keggfc:14.2] [sgdfc:3.3.0]
CONTIG5814	26737503_f2_14	4521	18624	381	127	YAR007C	303	2.8(10)-26	Saccharomyces cerevisiae	[ui:yar007c] [pn:dna replication factor a, 69 kd subunit:replication factor-a protein 1:rf-a:single-stranded dna-binding protein:dna binding protein buf2] [gn:rfal:buf2:rpal:fun3] [gtcf:10.1:10.2:10.8:12.9] [keggfc:14.2] [sgdfc:3.3.0]
CONTIG5688	24242181_f3_13	4522	18625	1575	525	YBL103C	134	3.5(10)-6	Saccharomyces cerevisiae	[ui:ybl103c] [pn:bhlh/zip transcription factor that regulates cit2 gene expression:retrograde regulation protein 3] [gn:rtg3:ybl0810] [gtcf:10.1:10.2:12.13] [keggfc:14.2] [sgdfc:1.5.2.4.8.2.9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3479	4722510_f1_1	4523	18626	513	171	YBL093C	151	5.9(10)-11	Saccharomyces cerevisiae	[ui:ybl093c] [pn:transcription factor:rox3 nuclear protein] [gn:rox3:ybl0837] [gtcf:10.1:10.2:13.2] [keggf:14.2] [sgdfc:4.8:2.9:5.0:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5561	19565875_c3_16	4524	18627	2646	882	YBL084C	698	6.0(10)-86	Saccharomyces cerevisiae	[ui:ybl084c] [pn:subunit of anaphase-promoting complex:cyclosome:cell division control protein 27] [gn:cdc27:snb1:ybl0718] [gtcf:10.1:10.11:10.2:12.16:12.8] [keggf:14.2] [sgdfc:3.8:0.6:5.1:9.3:0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1136	10962752_c3_3	4525	18628	735	245	YBL079W	227	1.8(10)-17	Saccharomyces cerevisiae	[ui:ybl079w] [pn:nuclear pore protein:nucleoporin nup170:nuclear pore protein nup170] [gn:nup170:ybl0725] [gtcf:10.1:10.2:12.6] [keggf:14.2] [sgdfc:8.1:0.9:5.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2309	2131950_f3_2	4526	18629	609	203	YBL079W	169	2.7(10)-11	Saccharomyces cerevisiae	[ui:ybl079w] [pn:nuclear pore protein:nucleoporin nup170:nuclear pore protein nup170] [gn:nup170:ybl0725] [gtcf:10.1:10.2:12.6] [keggf:14.2] [sgdfc:8.1:0.9:5.0:17.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2594	24422162_c1_3	4527	18630	612	204	YBL079W	328	3.2(10)-28	Saccharomyces cerevisiae	[ui:ybl079w] [pn:nuclear pore protein:nucleoporin nup170:nuclear pore protein nup170] [gn:nup170:ybl072.5] [gtcf:10.1:10.2:12.6] [keggf:14.2] [sgdf:8.1.0:9.5.0:17.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2791	23563513_f3_1	4528	18631	1230	410	YBL063W	683	1.3(10)-66	Saccharomyces cerevisiae	[ui:ybl063w] [pn:kinesin-related protein:kinesin-like protein kip1] [gn:kip1:cin9:ybl0504:ybl0521] [gtcf:10.1:10.2:12.16:12.8] [keggf:14.2] [sgdf:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5586	12614033_c1_16	4529	18632	1692	564	YBL063W	402	2.5(10)-36	Saccharomyces cerevisiae	[ui:ybl063w] [pn:kinesin-related protein:kinesin-like protein kip1] [gn:kip1:cin9:ybl0504:ybl0521] [gtcf:10.1:10.2:12.16:12.8] [keggf:14.2] [sgdf:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4385	14876506_f2_4	4530	18633	462	154	YBL035C	110	6.5(10)-5	Saccharomyces cerevisiae	[ui:ybl035c] [pn:subunit of dna polymerase alpha:primase complex:dna polymerase alpha/primase associated subunit:p86 subunit] [gn:pol12:ybl0414] [gtcf:10.1:10.2:10.8] [keggf:14.2] [sgdf:3.6.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4737	203251_c3_5	4531	18634	1131	377	YBL035C	725	8.9(10)-72	Saccharomyces cerevisiae	[ui:ybl035c] [pn:subunit of dna polymerase alpha-primase complex:dna polymerase alpha/primase associated subunit:p86 subunit] [gn:pol12:ybl0414] [gtcf:10.1:10.2:10.8] [keggf:14.2] [sgdfc:3.6:0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4470	23470317_c3_8	4532	18635	375	125	YBL026W	367	7.7(10)-34	Saccharomyces cerevisiae	[ui:ybl026w] [pn:snmp-related protein:hypothetical 11.2 kd protein in rp119-mcm2 intergenic region] [gn:snp3:ybl0425] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4772	14555312_f2_3	4533	18636	2061	687	YBL024W	1801	8.5(10)-186	Saccharomyces cerevisiae	[ui:ybl024w] [pn:similarity to nucleolar nop2p:hypothetical 77.9 kd protein in rm10-mcm2 intergenic region] [gn:ybl0437] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:9.5.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4940	58532_f2_1	4534	18637	1635	545	YBL023C	1691	4.9(10)-218	Saccharomyces cerevisiae	[ui:ybl023c] [pn:member of the mcm2p,mcm3p,cdc46p family:minichromosome maintenance protein 2] [gn:mcm2:ybl0438] [gtcf:10.1:10.2:10.8:12.8] [keggf:13.2] [sgdfc:3.6:0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1248	12209752_f2_1	4535	18638	660	220	YBL021C	303	4.5(10)-27	Saccharomyces cerevisiae	[ui:ybl021c] [pn:ccat-binding factor subunit:hap3 transcriptional activator:uas2 regulatory protein a] [gn:hap3:ybl0441] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5141	4104637_f2_1	4536	18639	330	110	YBL021C	413	1.0(10)-38	Saccharomyces cerevisiae	[ui:ybl021c] [pn:ccat-binding factor subunit:hap3 transcriptional activator:uas2 regulatory protein a] [gn:hap3:ybl0441] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2073	4772630_f2_1	4537	18640	1425	475	YBL020W	422	1.1(10)-39	Saccharomyces cerevisiae	[ui:ybl020w] [pn:nuclear division protein:nuclear division rft1 protein] [gn:rft1:ybl0442] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5197	10001885_f3_1	4538	18641	2436	812	YBL014C	219	2.8(10)-14	Saccharomyces cerevisiae	[ui:ybl014c] [pn:rna polymerase i specific transcription initiation factor:rna polymerase i specific transcription initiation factor rm6] [gn:rm6:ybl0311:ybl0312] [gtcf:10.1:10.2:10.3] [keggf:14.2] [sgdfc:4.1.0:9.5.0] [db:gtc-sacc

CONTIG3645	4711636_f3_3	4539	18642	1263	421	YBL008W	1125	3.6(10)-114	Saccharomyces cerevisiae	[ui:ybl008w] [pn:histone transcription regulator 1] [gn:hrl1:ybl0318] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4343	782806_c3_9	4540	18643	1404	468	YBL008W	101	0.07299	Saccharomyces cerevisiae	[ui:ybl008w] [pn:histone transcription regulator:histone transcription regulator 1] [gn:hrl1:ybl0318] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5245	5080340_c3_21	4541	18644	1467	489	YBL008W	189	9.5(10)-15	Saccharomyces cerevisiae	[ui:ybl008w] [pn:histone transcription regulator:histone transcription regulator 1] [gn:hrl1:ybl0318] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2490	10976555_f1_2	4542	18645	324	108	YBR009C	383	1.5(10)-35	Saccharomyces cerevisiae	[ui:ybr009c] [pn:histone h4] [gn:hhf1:ybr0122:hhf2:n2752] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5534	23437687_f2_6	4543	18646	348	116	YBR009C	384	1.2(10)-35	Saccharomyces cerevisiae	[ui:ybr009c] [pn:histone h4] [gn:hhf1:ybr0122:hhf2:n2752] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1485	16032090_f2_2	4544	18647	507	169	YBR010W	324	2.7(10)-29	Saccharomyces cerevisiae	[ui:ybr010w] [pn:histone h3] [gn:hht1:ybr0201:hht2:sin2:n2749] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2687	34250313_c3_3	4545	18648	261	87	YBR010W	387	5.7(10)-36	Saccharomyces cerevisiae	[ui:ybr010w] [pn:histone h3] [gn:hht1:ybr0201:hht2:sin2:n2749] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5534	19531300_c3_18	4546	18649	459	153	YBR010W	647	1.6(10)-63	Saccharomyces cerevisiae	[ui:ybr010w] [pn:histone h3] [gn:hht1:ybr0201:hht2:sin2:n2749] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2229	26378503_fl_1	4547	18650	471	157	YBR026C	318	1.2(10)-28	Saccharomyces cerevisiae	[ui:ybr026c] [pn:mitochondrial respiratory function protein:mitochondrial respiratory function protein 1] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4624	3305317_f3_4	4548	18651	1185	395	YBR026C	507	1.1(10)-48	Saccharomyces cerevisiae	[ui:ybr026c] [pn:mitochondrial respiratory function protein:mitochondrial respiratory function protein 1] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1160	22695943_c1_4	4549	18652	240	80	YBR049C	113	2.7(10)-14	Saccharomyces cerevisiae	[ui:ybr049c] [pn:transcription factor:dna-binding protein reb1:qbp] [gn:reb1:grf2:ybr0502] [gtcf:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.1.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5208	25476516_c2_14	4550	18653	1185	395	YBR055C	462	5.4(10)-43	Saccharomyces cerevisiae	[ui:ybr055c] [pn:snmp.u4/u6-associated splicing factor:pre-mma splicing factor prp6] [gn:prp6:ma6:ybr0508] [gtfc:10.1:10.2] [keggc:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5208	22854652_c2_13	4551	18654	747	249	YBR055C	180	9.9(10)-13	Saccharomyces cerevisiae	[ui:ybr055c] [pn:snmp.u4/u6-associated splicing factor:pre-mma splicing factor prp6] [gn:prp6:ma6:ybr0508] [gtfc:10.1:10.2] [keggc:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
b2x12464.x	4860050_c3_1	4552	18655	603	201	YBR055C	246	8.5(10)-20	Saccharomyces cerevisiae	[ui:ybr055c] [pn:snmp.u4/u6-associated splicing factor:pre-mma splicing factor prp6] [gn:prp6:ma6:ybr0508] [gtfc:10.1:10.2] [keggc:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3320	11750817_f3_3	4553	18656	1242	414	YBR060C	602	9.5(10)-59	Saccharomyces cerevisiae	[ui:ybr060c] [pn:origin recognition complex, 72 kda subunit:origin recognition complex protein, subunit 2:origin recognition complex protein 71 kd subunit] [gn:orc2:rr1:sir5:ybr0523] [gtfc:10.1:10.2:10.8:12.8:12.9] [keggc:13.2] [sg

CONTIG3647	41562877_c1_3	4554	18657	318	106	YBR081C	107	9.6(10)-5	Saccharomyces cerevisiae	[ui:ybr081c] [pn:involved in alteration of transcriptional start site selection:transcriptional activator spt7] [gn:spt7:ybr0739] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4860	26343875_f3_4	4555	18658	3006	1002	YBR081C	662	1.2(10)-135	Saccharomyces cerevisiae	[ui:ybr081c] [pn:involved in alteration of transcriptional start site selection:transcriptional activator spt7] [gn:spt7:ybr0739] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4671	4098513_f2_2	4556	18659	1347	449	YBR083W	213	1.0(10)-14	Saccharomyces cerevisiae	[ui:ybr083w] [pn:ty transcription activator:ty transcription activator tec1] [gn:tec1:roc1:ybr0750] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.2.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1943	2822192_f1_1	4557	18660	261	87	YBR087W	141	3.2(10)-9	Saccharomyces cerevisiae	[ui:ybr087w] [pn:dna replication factor c, 40 kd subunit:activator 1 subunit 5:replication factor c subunit 5] [gn:rfc5:ybr0810] [gtcf:10.1:10.2:10.8] [keggf:14.2] [sgdfc:3.6.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
b3x19517.y	25652036_f2_1	4558	18661	870	290	YBR087W	692	2.7(10)-68	Saccharomyces cerevisiae	[ui:ybr087w] [pn:dna replication factor c, 40 kd subunit:activator 1 subunit 5:replication factor c subunit 5] [gn:rfc5:ybr0810] [gtcf:10.1:10.2:10.8] [keggf:14.2] [sgdfc:3.6.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2521	23939051_c2_9	4559	18662	798	266	YBR088C	740	2.2(10)-73	Saccharomyces cerevisiae	[lui:ybr088c] [pn:proliferating cell nuclear antigen:pcna] [gn:pol30:ybr0811] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6:0.3:7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4482	35633436_f3_7	4560	18663	2001	667	YBR112C	1362	2.7(10)-139	Saccharomyces cerevisiae	[lui:ybr112c] [pn:general repressor of transcription:glucose repression mediator protein] [gn:ssn6:cyc8:ybr0908] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9.5.0] [db:gtc-saccharomyces cerevisiae]
b3x16071.y	36147808_c3_4	4561	18664	303	101	YBR112C	116	7.4(10)-6	Saccharomyces cerevisiae	[lui:ybr112c] [pn:general repressor of transcription:glucose repression mediator protein] [gn:ssn6:cyc8:ybr0908] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9.5.0] [db:gtc-saccharomyces cerevisiae]
b3x13452.y	24635752_c3_2	4562	18665	606	202	YBR112C	108	0.0018	Saccharomyces cerevisiae	[lui:ybr112c] [pn:general repressor of transcription:glucose repression mediator protein] [gn:ssn6:cyc8:ybr0908] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4298	22065680_f1_1	4563	18666	3207	1069	YBR114W	130	4.2(10)-7	Saccharomyces cerevisiae	[lui:ybr114w] [pn:nucleotide excision repair protein:dna repair protein rad16] [gn:rad16:ybr0909] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.7:0:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5782	5256282_cl_18	4564	18667	2568	856	YBR114W	2633	5.7(10)-274	Saccharomyces cerevisiae	[ui:ybr114w] [pn:nucleotide excision repair protein:dna repair protein rad16] [gn:rad16:ybr0909] [gtcf:10.1:10.10.2:10.8] [keggfc:14.2] [sgdfe:3.7.0:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG863	14722182_cl_2	4565	18668	435	145	YBR123C	171	5.5(10)-12	Saccharomyces cerevisiae	[ui:ybr123c] [pn:tftiic:transcription initiation factor subunit, 95 kd:transcription factor tau 95 kd subunit:tftiic 95 kd subunit] [gn:tftc1:ybr0919] [gtcf:10.1:10.2:10.3] [keggfc:14.2] [sgdfe:4.1.0:4.4.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2869	22089187_f3_1	4566	18669	1095	365	YBR150C	91	0.53	Saccharomyces cerevisiae	[ui:ybr150c] [pn:weak similarity to transcription factors:putative 126.9 kd transcriptional regulatory protein in ysw1-rib7 intergenic region] [gn:ybr1133] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfe:4.12.0:9.5.0] [db:gtc-saccharomyces cer]
CONTIG3753	26274013_fl_1	4567	18670	1422	474	YBR198C	1260	1.8(10)-128	Saccharomyces cerevisiae	[ui:ybr198c] [pn:tftid subunit:trp-aspartate repeats containing protein in pgil1- ktr4 intergenic region] [gn:tar90:ybr1410] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfe:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5005	22066557_c2_4	4568	18671	1182	394	YBR198C	215	1.3(10)-14	Saccharomyces cerevisiae	[ui:ybr198c] [pn:tfiid subunit:trp-asp repeats containing protein in pgil - ktr4 intergenic region] [gn:taf90:ybr1410] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:4.8.1:9.5.0] [db:gtc-saccharomyces]
CONTIG5810	22438777_b3_21	4569	18672	864	288	YBR198C	199	1.0(10)-27	Saccharomyces cerevisiae	[ui:ybr198c] [pn:tfiid subunit:trp-asp repeats containing protein in pgil - ktr4 intergenic region] [gn:taf90:ybr1410] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:4.8.1:9.5.0] [db:gtc-saccharomyces]
CONTIG2640	13683587_c1_2	4570	18673	996	332	YBR202W	1238	3.8(10)-126	Saccharomyces cerevisiae	[ui:ybr202w] [pn:cell division control protein:cell division control protein 47] [gn:cde47:ybr1441] [gtcf:10.1:10.2:10.8:12.8] [keggf:14.2] [sgdf:3.6.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4638	16222813_c1_8	4571	18674	948	316	YBR202W	362	2.7(10)-32	Saccharomyces cerevisiae	[ui:ybr202w] [pn:cell division control protein:cell division control protein 47] [gn:cde47:ybr1441] [gtcf:10.1:10.2:10.8:12.8] [keggf:14.2] [sgdf:3.6.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4195	6355200_c1_3	4572	18675	2007	669	YBR237W	1067	5.0(10)-108	Saccharomyces cerevisiae	[ui:ybr237w] [pn:pre-mrna processing ma-helicase:prp5] [gn:prp5:ma5:ybr1603] [gtcf:10.1:10.2:12.16] [keggfc:14.2] [sgdfc:4.9.0:6.4.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2066	19546878_c1_2	4573	18676	942	314	YBR239C	173	3.7(10)-14	Saccharomyces cerevisiae	[ui:ybr239c] [pn:weak similarity to transcription factor put3p:putative 60.3 kd transcriptional regulatory protein in prp5-alg7 intergenic region] [gn:ybr1622] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2225	34423436_c2_2	4574	18677	294	98	YBR239C	248	1.8(10)-20	Saccharomyces cerevisiae	[ui:ybr239c] [pn:weak similarity to transcription factor put3p:putative 60.3 kd transcriptional regulatory protein in prp5-alg7 intergenic region] [gn:ybr1622] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4191	20423138_c3_7	4575	18678	1941	647	YBR239C	243	5.7(10)-26	Saccharomyces cerevisiae	[ui:ybr239c] [pn:weak similarity to transcription factor put3p:putative 60.3 kd transcriptional regulatory protein in prp5-alg7 intergenic region] [gn:ybr1622] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5697	20081537_f3_10	4576	18679	2427	809	YBR239C	104	0.035	Saccharomyces cerevisiae	[lui:ybr239c] [pn:weak similarity to transcription factor put3p:putative 60.3 kd transcriptional regulatory protein in prp5-alg7 intergenic region] [gn:ybr1622] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5532	211507_f1_1	4577	18680	351	117	YBR247C	334	2.3(10)-30	Saccharomyces cerevisiae	[lui:ybr247c] [pn:n-glycosylation protein:enp1 protein] [gn:enp1:meg1:ybr1635] [gtcf:10.1:10.2:10.7] [keggfc:14.2] [sgdfc:6.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4398	31292707_f3_2	4578	18681	645	215	YBR275C	90	0.54	Saccharomyces cerevisiae	[lui:ybr275c] [pn:rif1 protein:rap1-interacting factor 1] [gn:rif1:ybr1743] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4398	11719762_f1_1	4579	18682	1779	593	YBR275C	104	4.9(10)-7	Saccharomyces cerevisiae	[lui:ybr275c] [pn:rif1 protein:rap1-interacting factor 1] [gn:rif1:ybr1743] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3103	30585057_f3_2	4580	18683	1446	482	YBR279W	260	9.5(10)-30	Saccharomyces cerevisiae	[lui:ybr279w] [pn:dna-directed ma polymerase ii regulator:pafl protein] [gn:pafl:ybr2016] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2336	437512_f1_1	4581	18684	1311	437	YBR289W	309	6.9(10)-30	Saccharomyces cerevisiae	[ui:ybr289w] [pn:component of swi/snf transcription activator complex:transcription regulatory protein snf5:swi/snf complex component snf5:transcription factor tye4] [gn:snf5:tye4:swi10:ybr2036] [gtcf:10.1:10.2:12.13:12.9] [keggfc:14
CONTIG3809	2355208_f3_4	4582	18685	669	223	YBR289W	278	3.2(10)-23	Saccharomyces cerevisiae	[ui:ybr289w] [pn:component of swi/snf transcription activator complex:transcription regulatory protein snf5:swi/snf complex component snf5:transcription factor tye4] [gn:snf5:tye4:swi10:ybr2036] [gtcf:10.1:10.2:12.13:12.9] [keggfc:14
CONTIG2911	24015625_f2_3	4583	18686	636	212	YCL066W	106	0.00013	Saccharomyces cerevisiae	[ui:ycl066w] [pn:mating type regulatory protein, silenced copy at hml:1 mating type regulatory protein, expressed copy at mat locus:mating-type protein alpha-1] [gn:alpha1:matalpha:ycl66w:matal1:mat1a:mat_alpha-1:ycr40w] [gtcf:10.1:10

CONTIG5663	6645262_c2_15	4584	18687	987	329	YCL055W	828	1.3(10)-86	Saccharomyces cerevisiae	[ui:ycl055w] [pn:regulatory protein required for pheromone induction of karyogamy genes:hypothetical 38.7 kd protein in prd1-pbn1 intergenic region] [gn:kar4:ycl55w:ycl432] [gtcf:10.1:10.2:12.9] [keggfc:14.2] [sgdfc:3.3.0:4.8.2:9.5.0]
CONTIG353	36360326_f2_1	4585	18688	249	83	YCL054W	409	1.3(10)-37	Saccharomyces cerevisiae	[ui:ycl054w] [pn:transcriptional silencing protein:hypothetical 83.2 kd protein in prd1-pbn1 intergenic region] [gn:ycl54w:ycl431] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5623	36360326_fl_1	4586	18689	1536	512	YCL054W	1258	1.3(10)-176	Saccharomyces cerevisiae	[ui:ycl054w] [pn:transcriptional silencing protein:hypothetical 83.2 kd protein in prd1-pbn1 intergenic region] [gn:ycl54w:ycl431] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3731	10567301_c2_16	4587	18690	375	125	YCL029C	159	5.7(10)-11	Saccharomyces cerevisiae	[ui:ycl029c] [pn:nuclear fusion protein:nuclear fusion protein bik1] [gn:bik1:ycl29c] [gtcf:10.1:10.2:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:3.3.0:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5143	26741377_c1_15	4588	18691	1287	429	YCL011C	413	5.5(10)-63	Saccharomyces cerevisiae	[ui:ycl011c] [pn:potential telomere-associated protein:single-strand telomeric dna-binding protein gbp2:g-strand binding protein 2:rap1 localization factor 6] [gn:gbp2:rlf6:ycl11c] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:9.5:0:9.6:0] [
CONTIG3208	35723780_fl_1	4589	18692	1158	386	YCR042C	379	1.1(10)-33	Saccharomyces cerevisiae	[ui:ycr042c] [pn:component of taf:ii complex:tsm1 protein] [gn:tsm1:ycr42c:ycr724] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3956	26054813_c2_8	4590	18693	1443	481	YCR042C	879	2.7(10)-87	Saccharomyces cerevisiae	[ui:ycr042c] [pn:component of taf:ii complex:tsm1 protein] [gn:tsm1:ycr42c:ycr724] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3956	4800906_c3_9	4591	18694	663	221	YCR042C	212	6.9(10)-16	Saccharomyces cerevisiae	[ui:ycr042c] [pn:component of taf:ii complex:tsm1 protein] [gn:tsm1:ycr42c:ycr724] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3956	4007160_c3_10	4592	18695	189	63	YCR042C	144	1.2(10)-8	Saccharomyces cerevisiae	[ui:ycr042c] [pn:component of taf:ii complex:tsm1 protein] [gn:tsm1:ycr42c:ycr724] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9.5:0] [db:gtc-saccharomyces cerevisiae]

CONTIG4152	24414083_f1_2	4593	18696	720	240	YCR065W	266	2.0(10)-22	Saccharomyces cerevisiae	[ui:ycr065w] [pn:transcription factor:hcm1 protein] [gn:hcm1:ycr65w:ycr902] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5596	23609536_f3_11	4594	18697	777	259	YCR065W	103	0.0074	Saccharomyces cerevisiae	[ui:ycr065w] [pn:transcription factor:hcm1 protein] [gn:hcm1:ycr65w:ycr902] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5184	12140677_c2_11	4595	18698	1176	392	YCR066W	247	1.5(10)-34	Saccharomyces cerevisiae	[ui:ycr066w] [pn:dna repair protein:dna repair protein rad18] [gn:rad18:ycr66w] [gtcf:10.1:10.10:10.2:10.8] [keggf:14.2] [sgdfc:3.7.0:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1568	4094567_c3_4	4596	18699	942	314	YCR072C	106	0.00459	Saccharomyces cerevisiae	[ui:ycr072c] [pn:beta-transducin family:wd-40 repeat protein:hypothetical trp-asp repeats containing protein in cpr4- ssk22 intergenic region] [gn:ycr72c] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:9.5.0:13.0.0] [db:gtc-saccharomyces cere]
CONTIG5040	13688762_c2_13	4597	18700	1224	408	YCR072C	122	0.00017	Saccharomyces cerevisiae	[ui:ycr072c] [pn:beta-transducin family:wd-40 repeat protein:hypothetical trp-asp repeats containing protein in cpr4- ssk22 intergenic region] [gn:ycr72c] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:9.5.0:13.0.0] [db:gtc-saccharomyces cere]

CONTIG708	24797506_c2_4	4598	18701	993	331	YCR072C	1156	1.8(10)-117	Saccharomyces cerevisiae	[ui:ycr072c] [pn:beta-transducin family:wd-40 repeat protein:hypothetical trp-aspartate repeats containing protein in cpr4-ssk22 intergenic region] [gn:ycr72c] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:9.5.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
b9x10155.y	23693849_c1_2	4599	18702	471	157	YCR072C	594	6.7(10)-58	Saccharomyces cerevisiae	[ui:ycr072c] [pn:beta-transducin family:wd-40 repeat protein:hypothetical trp-aspartate repeats containing protein in cpr4-ssk22 intergenic region] [gn:ycr72c] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:9.5.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5601	12238550_f1_1	4600	18703	1185	395	YCR084C	1050	3.2(10)-106	Saccharomyces cerevisiae	[ui:ycr084c] [pn:general transcription repressor:glucose repression regulatory protein tup1:flocculation suppressor protein:repressor aer2] [gn:tup1:aer2:slf2:cyc9:umr7:aar1:amml1:flk1_orycr84c] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:4]
CONTIG1665	8392_c1_2	4601	18704	690	230	YCR092C	274	1.1(10)-22	Saccharomyces cerevisiae	[ui:ycr092c] [pn:dna mismatch repair protein:mismatch binding protein homolog 3:mismatch binding protein:mbp] [gn:msh3:ycr92c:ycr1152] [gtcf:10.1:10.2:10.8] [keggf:14.2] [sgdf:3.7.0.9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3957	2789050_f3_4	4602	18705	234	78	YCR092C	98	0.00067	Saccharomyces cerevisiae	[ui:ycr092c] [pn:dna mismatch repair protein:mut protein homolog 3:mismatch binding protein:mbp] [gn:msh3:ycr92c:ycr1152] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3957	14178130_f1_1	4603	18706	897	299	YCR092C	597	2.2(10)-57	Saccharomyces cerevisiae	[ui:ycr092c] [pn:dna mismatch repair protein:mut protein homolog 3:mismatch binding protein:mbp] [gn:msh3:ycr92c:ycr1152] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1046	13882630_f2_1	4604	18707	675	225	YCR093W	345	8.0(10)-30	Saccharomyces cerevisiae	[ui:ycr093w] [pn:nuclear transmembrane protein:general negative regulator of transcription subunit 1] [gn:ntl:cde39:ros1:ycr93w:ycr1151] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1046	203575_f2_2	4605	18708	282	94	YCR093W	111	6.0(10)-5	Saccharomyces cerevisiae	[ui:ycr093w] [pn:nuclear transmembrane protein:general negative regulator of transcription subunit 1] [gn:ntl:cde39:ros1:ycr93w:ycr1151] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1166	176567_c3_4	4606	18709	957	319	YCR093W	602	3.7(10)-57	Saccharomyces cerevisiae	[ui:ycr093w] [pn:nuclear transmembrane protein:general negative regulator of transcription subunit 1] [gn:not1:cdc39:ros1:ycr93w:ycr115 1] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG895	24398311_f2_2	4607	18710	486	162	YCR093W	224	5.9(10)-17	Saccharomyces cerevisiae	[ui:ycr093w] [pn:nuclear transmembrane protein:general negative regulator of transcription subunit 1] [gn:not1:cdc39:ros1:ycr93w:ycr115 1] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG895	3150012_f1_1	4608	18711	678	226	YCR093W	220	1.6(10)-16	Saccharomyces cerevisiae	[ui:ycr093w] [pn:nuclear transmembrane protein:general negative regulator of transcription subunit 1] [gn:not1:cdc39:ros1:ycr93w:ycr115 1] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3229	4332802_f3_4	4609	18712	1761	587	YCR106W	142	3.7(10)-6	Saccharomyces cerevisiae	[ui:ycr106w] [pn:weak similarity to transcription factor pip2p:putative 95.7 kd transcriptional regulatory protein in pau3 3"region] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3945	2375030_c2_4	4610	18713	543	181	YDL226C	515	1.6(10)-49	Saccharomyces cerevisiae	[ui:ydl226c] [pn:cell proliferation zinc finger protein:zinc finger protein] [gn:gcs1] [gtcf:10.1:10.2:12.10:12.6:12.8] [keggf:14.2] [sgdfc:3.8.0:8.6.0:8.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5742	23609806_f3_14	4611	18714	1542	514	YDL207W	666	1.6(10)-65	Saccharomyces cerevisiae	[ui:ydl207w] [pn:ma export mediator] [gn:gle1] [gtcf:10.1:10.2:12.3] [keggf:14.2] [sgdfc:4.11.0:8.1.0:9.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3352	2156415_c1_3	4612	18715	558	186	YDL200C	258	2.7(10)-22	Saccharomyces cerevisiae	[ui:ydl200c] [pn:o6-methylguanine dna repair methyltransferase:methylated-dna--protein-cysteine methyltransferase:6-o-methylguanine-dna methyltransferase] [gn:mgt1:d1204] [gtcf:10.1:10.10:10.2:14.1] [ec:2.1.1.63] [keggf:14.1] [sgdfc
CONTIG5437	24350687_c3_23	4613	18716	561	187	YDL165W	324	2.7(10)-29	Saccharomyces cerevisiae	[ui:ydl165w] [pn:transcription factor:general negative regulator of transcription subunit 2] [gn:not2:cdc36:dna19] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.8.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5390	12896936_c1_14	4614	18717	198	66	YDL164C	112	1.5(10)-5	Saccharomyces cerevisiae	[ui:ydl164c] [pn:dna ligase:polydeoxyribonucleotide synthase:atp] [gn:cdc9] [gtcf:10.1:10.10:10.2:10.8:14.1] [ec:6.5.1.1] [keggf:14.1] [sgdfc:3.6.0:3.7.0:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5736	203942_c3_27	4615	18718	939	313	YDL164C	1025	1.3(10)-103	Saccharomyces cerevisiae	[ui:ydl164c] [pn:dna ligase:polydeoxyribonucleotide synthase:atp] [gn:cdc9] [gtcf:10.1:10.10:10.2:10.8:14.1] [ec:6.5.1.1] [keggf:14.1] [sgdfc:3.6.0:3.7.0:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2856	23570399_c1_4	4616	18719	1107	369	YDL164C	693	2.2(10)-68	Saccharomyces cerevisiae	[ui:ydl164c] [pn:dna ligase:polydeoxyribonucleotide synthase:atp] [gn:cdc9] [gtcf:10.1:10.10:10.2:10.8:14.1] [ec:6.5.1.1] [keggf:14.1] [sgdfc:3.6.0:3.7.0:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2033	2234792_fl_1	4617	18720	1149	383	YDL160C	1002	3.8(10)-101	Saccharomyces cerevisiae	[ui:ydl160c] [pn:strong similarity to rna helicases of the dead box family:putative atp-dependent rna helicase] [gn:dhhl] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3197	33209375_fl_2	4618	18721	621	207	YDL160C	739	2.8(10)-73	Saccharomyces cerevisiae	[ui:ydl160c] [pn:strong similarity to rna helicases of the dead box family:putative atp-dependent rna helicase] [gn:dhhl] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5717	12695903_c1_8	4619	18722	1725	575	YDL154W	702	2.3(10)-69	Saccharomyces cerevisiae	[ui:ydl154w] [pn:meiosis-specific protein] [gn:msh5] [gtfc:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.5.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1929	23597567_f1_1	4620	18723	981	327	YDL116W	179	1.2(10)-25	Saccharomyces cerevisiae	[ui:ydl116w] [pn:nucleoporin:nuclear pore protein] [gn:nup84] [gtfc:10.1:10.2] [keggfc:14.2] [sgdgc:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4692	14506511_f3_5	4621	18724	1479	493	YDL106C	339	6.0(10)-44	Saccharomyces cerevisiae	[ui:ydl106c] [pn:homeodomain protein:regulatory protein pho2:general regulatory factor 10] [gn:pho2:bas2:grf10:d2350] [gtfc:10.1:10.2:12.8:13.10] [keggfc:13.2] [sgdgc:1.3.5:1.4.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2064	10366327_f2_1	4622	18725	201	67	YDL056W	184	3.2(10)-13	Saccharomyces cerevisiae	[ui:ydl056w] [pn:transcription factor, subunit of the mbf factor:transcription factor:mbf subunit p120] [gn:mbp1] [gtfc:10.1:10.2:12.8] [keggfc:13.2] [sgdgc:3.8.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3259	20751657_c1_4	4623	18726	555	185	YDL056W	282	1.1(10)-23	Saccharomyces cerevisiae	[ui:ydl056w] [pn:transcription factor, subunit of the mbf factor:transcription factor:mbf subunit p120] [gn:mbp1] [gtfc:10.1:10.2:12.8] [keggfc:13.2] [sgdgc:3.8.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3884	20488905_f2_2	4624	18727	1461	487	YDL056W	95	0.28999	Saccharomyces cerevisiae	[ui:ydl056w] [pn:transcription factor, subunit of the mbf subunit p120] [gn:mbp1] [gtcf:10.1:10.2:12.8] [keggfc:13.2] [sgdfe:3.8.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4530	33789717_c1_8	4625	18728	2238	746	YDL056W	263	3.2(10)-25	Saccharomyces cerevisiae	[ui:ydl056w] [pn:transcription factor, subunit of the mbf subunit p120] [gn:mbp1] [gtcf:10.1:10.2:12.8] [keggfc:13.2] [sgdfe:3.8.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG973	22269759_c2_3	4626	18729	789	263	YDL056W	194	2.7(10)-14	Saccharomyces cerevisiae	[ui:ydl056w] [pn:transcription factor, subunit of the mbf subunit p120] [gn:mbp1] [gtcf:10.1:10.2:12.8] [keggfc:13.2] [sgdfe:3.8.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3237	4475386_c2_4	4627	18730	798	266	YDL043C	248	3.1(10)-21	Saccharomyces cerevisiae	[ui:ydl043c] [pn:pre-mrna splicing factor] [gn:prp11] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfe:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1026	12784405_f2_1	4628	18731	918	306	YDL030W	396	6.5(10)-37	Saccharomyces cerevisiae	[ui:ydl030w] [pn:pre-mrna splicing factor:snrna-associated protein:pre-mrna splicing factor prp9] [gn:prp9:d2773] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.9.0:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2121	29343840_f2_1	4629	18732	423	141	YDL030W	90	0.039	Saccharomyces cerevisiae	[ui:ydl030w] [pn:pre-mrna splicing factor:snrna-associated protein:pre-mrna splicing factor prp9] [gn:prp9:d2773] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.9.0:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2648	24851018_f3_2	4630	18733	1218	406	YDL020C	217	4.2(10)-17	Saccharomyces cerevisiae	[ui:ydl020c] [pn:nuclear protein:nuclear protein son1:ub fusion degradation protein 5] [gn:son1:ufd5:d2840] [gtcf:10.1:10.11:10.2] [keggf:14.2] [sgdfc:6.5.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5686	10759712_c2_23	4631	18734	1560	520	YDL020C	115	0.0014	Saccharomyces cerevisiae	[ui:ydl020c] [pn:nuclear protein:nuclear protein son1:ub fusion degradation protein 5] [gn:son1:ufd5:d2840] [gtcf:10.1:10.11:10.2] [keggf:14.2] [sgdfc:6.5.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5686	21890828_c3_27	4632	18735	1506	502	YDL020C	135	7.5(10)-6	Saccharomyces cerevisiae	[ui:ydl020c] [pn:nuclear protein:nuclear protein son1:ub fusion degradation protein 5] [gn:son1:ufd5:d2840] [gtcf:10.1:10.11:10.2] [keggf:14.2] [sgdfc:6.5.1:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3726	20312937_f1_1	4633	18736	480	160	YDL014W	774	5.7(10)-77	Saccharomyces cerevisiae	[ui:ydl014w] [pn:fibrillarin:nucleolar protein 1] [gn:nop1:d2870] [gtcf:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.2:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3726	12345187_f2_2	4634	18737	297	99	YDL014W	105	2.5(10)-5	Saccharomyces cerevisiae	[ui:ydl014w] [pn:fibrillarin:nucleolar protein 1] [gn:nop1:d2870] [gtcf:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.2:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5426	490917_f3_6	4635	18738	1557	519	YDR004W	252	2.7(10)-29	Saccharomyces cerevisiae	[ui:ydr004w] [pn:dna repair protein:dna repair protein rad57] [gn:rad57:ydr8119] [gtcf:10.1:10.10:10.2:10.8:12.8:12.9] [keggfc:14.2] [sgdfc:3.0:3.5:0.3:7.0:9.5:0.1:1.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4801	35803312_f3_5	4636	18739	1917	639	YDR006C	625	2.8(10)-98	Saccharomyces cerevisiae	[ui:ydr006c] [pn:high copy suppressor of a cyclic amp-dependent protein kinase mutant:sok1 protein] [gn:sok1:ydr8119] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9:5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1119	30250927_fl_1	4637	18740	756	252	YDR028C	107	3.0(10)-7	Saccharomyces cerevisiae	[ui:ydr028c] [pn:regulatory subunit for protein phosphatase glc7p:hex2 protein:srm1 protein:reg1 protein] [gn:hex2:srm1:reg1:spp43:ydr9813] [gtcf:10.1:10.2:12.13:12.8] [keggfc:13.1] [sgdfc:1.5.2:4.9.0:9.5.0] [db:gtc-saccharomyces cere
CONTIG2131	3929501_c1_3	4638	18741	621	207	YDR028C	105	0.00012	Saccharomyces cerevisiae	[ui:ydr028c] [pn:regulatory subunit for protein phosphatase glc7p:hex2 protein:srm1 protein:reg1 protein] [gn:hex2:srm1:reg1:spp43:ydr9813] [gtcf:10.1:10.2:12.13:12.8] [keggfc:13.1] [sgdfc:1.5.2:4.9.0:9.5.0] [db:gtc-saccharomyces cere
CONTIG2599	19632001_fl_1	4639	18742	1188	396	YDR028C	101	0.065	Saccharomyces cerevisiae	[ui:ydr028c] [pn:regulatory subunit for protein phosphatase glc7p:hex2 protein:srm1 protein:reg1 protein] [gn:hex2:srm1:reg1:spp43:ydr9813] [gtcf:10.1:10.2:12.13:12.8] [keggfc:13.1] [sgdfc:1.5.2:4.9.0:9.5.0] [db:gtc-saccharomyces cere

CONTIG2946	10833263_c3_7	4640	18743	1953	651	YDR028C	168	1.5(10)-11	Saccharomyces cerevisiae	[ui:ydr028c] [pn:regulatory subunit for protein phosphatase glc7p:hex2 protein:sm1 protein:reg1 protein] [gn:hex2:sm1:reg1:spp43:ydr9813] [gtcf:10.1:10.2:12.13:12.8] [keggfc:13.1] [sgdfc:1.5.2:4.9.0:9.5.0] [db:gtc-saccharomyces cere
CONTIG5418	19530_c3_20	4641	18744	222	74	YDR028C	117	6.0(10)-6	Saccharomyces cerevisiae	[ui:ydr028c] [pn:regulatory subunit for protein phosphatase glc7p:hex2 protein:sm1 protein:reg1 protein] [gn:hex2:sm1:reg1:spp43:ydr9813] [gtcf:10.1:10.2:12.13:12.8] [keggfc:13.1] [sgdfc:1.5.2:4.9.0:9.5.0] [db:gtc-saccharomyces cere
CONTIG554	29550762_f1_1	4642	18745	807	269	YDR028C	381	2.1(10)-43	Saccharomyces cerevisiae	[ui:ydr028c] [pn:regulatory subunit for protein phosphatase glc7p:hex2 protein:sm1 protein:reg1 protein] [gn:hex2:sm1:reg1:spp43:ydr9813] [gtcf:10.1:10.2:12.13:12.8] [keggfc:13.1] [sgdfc:1.5.2:4.9.0:9.5.0] [db:gtc-saccharomyces cere
CONTIG1778	11882013_c1_1	4643	18746	216	72	YDR034C	123	1.0(10)-6	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14:ydr9673] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2271	6821877_c1_3	4644	18747	948	316	YDR034C	103	0.0016	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14.yd9673] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4112	398442_c3_6	4645	18748	696	232	YDR034C	122	1.3(10)-5	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14.yd9673] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2366	35287503_f1_1	4646	18749	873	291	YDR034C	108	0.00479	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14.yd9673] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4015	4100626_f3_8	4647	18750	1917	639	YDR034C	113	0.0027	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14.yd9673] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4450	35970266_c2_9	4648	18751	1863	621	YDR034C	109	0.01099	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14:yd9673] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:1.1.2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5002	6898551_c1_11	4649	18752	579	193	YDR034C	162	6.9(10)-11	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14:yd9673] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:1.1.2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5632	20597288_f1_1	4650	18753	2145	715	YDR034C	289	3.2(10)-28	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14:yd9673] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:1.1.2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5632	33441375_f2_3	4651	18754	726	242	YDR034C	145	4.5(10)-9	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14:yd9673] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:1.1.2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5664	15751250_f3_6	4652	18755	1197	399	YDR034C	211	5.0(10)-24	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14:ydr0673] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5791	4957813_f3_18	4653	18756	2070	690	YDR034C	295	1.3(10)-31	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14:ydr0673] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5802	4402067_f1_1	4654	18757	786	262	YDR034C	116	0.00033	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14:ydr0673] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
b9x11r38.x	10751640_f2_1	4655	18758	672	224	YDR034C	90	0.22	Saccharomyces cerevisiae	[ui:ydr034c] [pn:transcriptional activator of lysine pathway genes:lysine biosynthesis regulatory protein lys14] [gn:lys14:ydr0673] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2456	24323411_c3_4	4656	18759	1194	398	YDR052C	340	3.0(10)-34	Saccharomyces cerevisiae	[ui:ydr052c] [pn:regulatory subunit for cdc7p protein kinase:dbf4 protein:dna52 protein] [gn:dbf4:dna52:ydr052c] [gdcf:10.1:10.2:10.8:12.8] [keggf:13.2] [sgdcf:3.6:0.3:8.0:9.5.0] [db:gdc-saccharomyces cerevisiae]
CONTIG3705	182761_c3_10	4657	18760	786	262	YDR054C	622	7.2(10)-61	Saccharomyces cerevisiae	[ui:ydr054c] [pn:ubiquitin-conjugating enzyme:e2-34 kd:ubiquitin-protein ligase:ubiquitin carrier protein:cell division control protein 34] [gn:ubc3:cdc34:dna6:ydr054c] [gdcf:10.1:10.11:10.2:10.7:10.8:12.8]
CONTIG611	4882186_c2_4	4658	18761	972	324	YDR088C	104	2.5(10)-8	Saccharomyces cerevisiae	[ui:ydr088c] [pn:pre-mrna splicing factor affecting 3' splice site choice:pre-mrna splicing factor slu7] [gn:slu7:d4483] [gdcf:10.1:10.2] [keggf:14.2] [sgdcf:4.9:0:9.5.0] [db:gdc-saccharomyces cerevisiae]
CONTIG3779	4178300_f3_12	4659	18762	1764	588	YDR097C	940	1.5(10)-94	Saccharomyces cerevisiae	[ui:ydr097c] [pn:dna mismatch repair protein] [gn:msh6] [gdcf:10.1:10.2:10.8] [keggf:14.2] [sgdcf:3.7:0:9.5.0] [db:gdc-saccharomyces cerevisiae]
CONTIG3779	978202_f3_13	4660	18763	1671	557	YDR097C	1524	1.8(10)-156	Saccharomyces cerevisiae	[ui:ydr097c] [pn:dna mismatch repair protein] [gn:msh6] [gdcf:10.1:10.2:10.8] [keggf:14.2] [sgdcf:3.7:0:9.5.0] [db:gdc-saccharomyces cerevisiae]

CONTIG5779	9946877_f1_3	4661	18764	261	87	YDR097C	142	1.7(10)-8	Saccharomyces cerevisiae	[ui:ydr097c] [pn:dna mismatch repair protein] [gn:msh6] [gicfc:10.1:10.2:10.8] [keggfc:14.2] [sgdgc:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4241	4772125_f1_2	4662	18765	1719	573	YDR159W	1095	5.5(10)-111	Saccharomyces cerevisiae	[ui:ydr159w] [pn:leucine permease transcriptional regulator] [gn:sac3:lep1:ydr8358] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG864	20901562_f2_2	4663	18766	711	237	YDR159W	210	1.0(10)-15	Saccharomyces cerevisiae	[ui:ydr159w] [pn:leucine permease transcriptional regulator] [gn:sac3:lep1:ydr8358] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4895	7206462_c3_6	4664	18767	954	318	YDR173C	463	5.2(10)-44	Saccharomyces cerevisiae	[ui:ydr173c] [pn:arginine metabolism transcription factor:arginine metabolism regulation protein iii] [gn:argr3:arg82:ydr9395] [gicfc:10.1:10.2:12.15] [keggfc:14.2] [sgdgc:1.1.2:3.4.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG969	24335417_c3_4	4665	18768	891	297	YDR176W	470	1.8(10)-44	Saccharomyces cerevisiae	[ui:ydr176w] [pn:general transcriptional adaptor or co-activator:ada3 protein:ngg1 protein] [gn:ada3:ngg1:ydr9395] [gicfc:10.1:10.2:12.13] [keggfc:14.2] [sgdgc:1.5.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1884	975012_fl_1	4666	18769	876	292	YDR217C	132	3.5(10)-6	Saccharomyces cerevisiae	[ui:ydr217c] [pn:dna repair checkpoint protein: dna repair protein] [gn:rad9] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3962	16835925_c2_7	4667	18770	399	133	YDR224C	466	2.5(10)-44	Saccharomyces cerevisiae	[ui:ydr224c] [pn:histone h2b:histone h2b.1] [gn:h2b1:h2b1:spt12:ydr9934] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:4.8.2:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4359	4741062_fl_1	4668	18771	549	183	YDR225W	518	7.7(10)-50	Saccharomyces cerevisiae	[ui:ydr225w] [pn:histone h2a:histone h2a.1] [gn:h2a1:h2a1:spt11:ydr9934] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:4.8.2:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3853	11117280_f3_4	4669	18772	1134	378	YDR228C	154	2.8(10)-22	Saccharomyces cerevisiae	[ui:ydr228c] [pn:component of pre-mrna 3'-end processing factor cf i] [gn:pcf1] [gtcf:10.1:10.2:10.9] [keggfc:14.2] [sgdgc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5337	4812525_f3_2	4670	18773	954	318	YDR228C	242	1.2(10)-19	Saccharomyces cerevisiae	[ui:ydr228c] [pn:component of pre-mrna 3'-end processing factor cf i] [gn:pcf1] [gtcf:10.1:10.2:10.9] [keggfc:14.2] [sgdgc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5312	9922131_f3_7	4671	18774	912	304	YDR216W	204	4.5(10)-15	Saccharomyces cerevisiae	[ui:ydr216w] [pn:zinc-finger transcription factor:regulatory protein adr1] [gn:adr1.yd8142] [gtcf:10.1:10.2:12.13] [keggf:14.2] [sgdf:1.5.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG927	11828957_f1_1	4672	18775	873	291	YDR216W	225	2.6(10)-17	Saccharomyces cerevisiae	[ui:ydr216w] [pn:zinc-finger transcription factor:regulatory protein adr1] [gn:adr1.yd8142] [gtcf:10.1:10.2:12.13] [keggf:14.2] [sgdf:1.5.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3333	13867037_c1_4	4673	18776	957	319	YDR243C	426	4.2(10)-40	Saccharomyces cerevisiae	[ui:ydr243c] [pn:pre-mrna splicing factor rna helicase of dead box family:pre-mrna splicing factor rna helicase prp28:helicase ca8] [gn:prp28.yd8419] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4458	11737891_c2_6	4674	18777	381	127	YDR243C	188	7.0(10)-14	Saccharomyces cerevisiae	[ui:ydr243c] [pn:pre-mrna splicing factor rna helicase of dead box family:pre-mrna splicing factor rna helicase prp28:helicase ca8] [gn:prp28.yd8419] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2065	167625_f3_2	4675	18778	591	197	YDR254W	140	7.0(10)-9	Saccharomyces cerevisiae	[ui:ydr254w] [pn:chromosome segregation protein:putative cell chl4] [gn:chl4:ctf17:y9320a] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4619	12506512_f2_4	4676	18779	564	188	YDR254W	208	2.8(10)-16	Saccharomyces cerevisiae	[ui:ydr254w] [pn:chromosome segregation protein:putative cell chl4] [gn:chl4:ctf17:y9320a] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG1848	10814002_c1_2	4677	18780	210	70	YDR257C	97	0.00034	Saccharomyces cerevisiae	[ui:ydr257c] [pn:regulatory protein] [gn:rmsl] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3873	120157_c2_3	4678	18781	1167	389	YDR257C	253	1.8(10)-40	Saccharomyces cerevisiae	[ui:ydr257c] [pn:regulatory protein] [gn:rmsl] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG1274	9797251_f1_1	4679	18782	762	254	YDR285W	94	0.14999	Saccharomyces cerevisiae	[ui:ydr285w] [pn:synaptonemal complex protein:synaptonemal complex protein zip1] [gn:zip1:d9819] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.5:0:3.8:0:9.5:0:9.6:0] [db:gtc-saccharomyces cerevisiae]

CONTIG4344	12118760_c2_8	4680	18783	543	181	YDR285W	113	0.00036	Saccharomyces cerevisiae	[ui:ydr285w] [pn:synaptonemal complex protein:zip1] [gn:zip1:d9819] [gfcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.5:0.3:8.0:9.5:0.9:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4822	30117187_c2_12	4681	18784	1350	450	YDR285W	106	0.023	Saccharomyces cerevisiae	[ui:ydr285w] [pn:synaptonemal complex protein:zip1] [gn:zip1:d9819] [gfcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.5:0.3:8.0:9.5:0.9:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5780	16147626_fl_1	4682	18785	405	135	YDR285W	93	0.01499	Saccharomyces cerevisiae	[ui:ydr285w] [pn:synaptonemal complex protein:zip1] [gn:zip1:d9819] [gfcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.5:0.3:8.0:9.5:0.9:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG270	10005011_c3_2	4683	18786	387	129	YDR301W	234	3.0(10)-18	Saccharomyces cerevisiae	[ui:ydr301w] [pn:pre-mrna 3"-end processing factor cf ii] [gn:cft1] [gfcf:10.1:10.2:10.9] [keggf:14.2] [sgdfc:4.10:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3074	4892288_c3_6	4684	18787	1587	529	YDR301W	694	4.5(10)-74	Saccharomyces cerevisiae	[ui:ydr301w] [pn:pre-mrna 3"-end processing factor cf ii] [gn:cft1] [gfcf:10.1:10.2:10.9] [keggf:14.2] [sgdfc:4.10:0.9:5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3248	29882938_f1_2	4685	18788	1107	369	YDR301W	185	8.5(10)-18	Saccharomyces cerevisiae	[ui:ydr301w] [pn:pre-mma 3"-end processing factor cf ii] [gn:cft1] [gtcf:10.1:10.2:10.9] [keggfc:14.2] [sgdfc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
b2x18140.y	26375442_f1_1	4686	18789	465	155	YDR301W	141	2.3(10)-8	Saccharomyces cerevisiae	[ui:ydr301w] [pn:pre-mma 3"-end processing factor cf ii] [gn:cft1] [gtcf:10.1:10.2:10.9] [keggfc:14.2] [sgdfc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4614	33773307_c2_6	4687	18790	672	224	YDR308C	165	2.0(10)-12	Saccharomyces cerevisiae	[ui:ydr308c] [pn:dna-directed mat polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit:suppressor of ma polymerase b srb7] [gn:srb7:d9740] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces c
CONTIG5785	7228218_c3_34	4688	18791	1716	572	YDR311W	433	6.4(10)-58	Saccharomyces cerevisiae	[ui:ydr311w] [pn:tffih subunit:transcription initiation factor, 75 kd:ma polymerase ii transcription factor b 73 kd subunit] [gn:tff1:d9740] [gtcf:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:4.8.1:9.5.0:11.2.1] [db:gtc-saccharomyces cerev

CONTIG5785	21875078_c1_24	4689	18792	423	141	YDR311W	125	4.7(10)-7	Saccharomyces cerevisiae	[ui:ydr311w] [pn:tfiih subunit:transcription initiation factor, 75 kd:ma polymerase ii transcription factor b 73 kd subunit] [gn:tfb1:d9740] [gtcf:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:4.8.1:9.5.0:11.2.1] [db:gtc-saccharomyces cerev
CONTIG4764	9782136_f1_1	4690	18793	549	183	YDR328C	469	1.5(10)-54	Saccharomyces cerevisiae	[ui:ydr328c] [pn:kinetochore protein complex cbf3, subunit d:centromere dna-binding protein complex cbf3 subunit d:suppressor of kinetochore protein 1] [gn:cbf3:d:skp1:d9798] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5.0:9.6.
CONTIG1200	1267200_f2_1	4691	18794	714	238	YDR356W	132	3.3(10)-6	Saccharomyces cerevisiae	[ui:ydr356w] [pn:spindle pole body component:nuf1 protein:spindle poly body spacer protein spc110] [gn:nuf1:spc110:d9476] [gtcf:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3798	2909500_t3_5	4692	18795	690	230	YDR356W	106	0.00719	Saccharomyces cerevisiae	[ui:ydr356w] [pn:spindle pole body component:nuf1 protein:spindle poly body spacer protein spc110] [gn:nuf1:spc110:d9476] [gtcf:10.1:10.2:12.16:12.8] [keggf:14.2] [sgdfc:3.8:0:9.3:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4570	4800451_t2_3	4693	18796	1449	483	YDR356W	102	0.05299	Saccharomyces cerevisiae	[ui:ydr356w] [pn:spindle pole body component:nuf1 protein:spindle poly body spacer protein spc110] [gn:nuf1:spc110:d9476] [gtcf:10.1:10.2:12.16:12.8] [keggf:14.2] [sgdfc:3.8:0:9.3:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4836	15042311_c3_6	4694	18797	900	300	YDR356W	98	0.095	Saccharomyces cerevisiae	[ui:ydr356w] [pn:spindle pole body component:nuf1 protein:spindle poly body spacer protein spc110] [gn:nuf1:spc110:d9476] [gtcf:10.1:10.2:12.16:12.8] [keggf:14.2] [sgdfc:3.8:0:9.3:0:9.5:0] [db:gtc-saccharomyces cerevisiae]

CONTIG4987	30352067_f3_3	4695	18798	2775	925	YDR356W	315	1.7(10)-24	Saccharomyces cerevisiae	[ui:ydr356w] [pn:spindle pole body component:nuf1 protein:spindle poly body spacer protein spc110] [gn:nuf1:spc110:d9476] [gtcf:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3315	991577_f3_5	4696	18799	1011	337	YDR356W	95	0.22	Saccharomyces cerevisiae	[ui:ydr356w] [pn:spindle pole body component:nuf1 protein:spindle poly body spacer protein spc110] [gn:nuf1:spc110:d9476] [gtcf:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5767	6034681_c1_33	4697	18800	2166	722	YDR356W	128	0.00017	Saccharomyces cerevisiae	[ui:ydr356w] [pn:spindle pole body component:nuf1 protein:spindle poly body spacer protein spc110] [gn:nuf1:spc110:d9476] [gtcf:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3581	954436_f1_1	4698	18801	813	271	YDR364C	451	2.7(10)-49	Saccharomyces cerevisiae	[ui:ydr364c] [pn:cell division control protein:cell division control protein 40] [gn:cdc40:xrs2] [gtcf:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.6.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2012	2922000_b3_2	4699	18802	984	328	YDR390C	685	7.7(10)-76	Saccharomyces cerevisiae	[ui:ydr390c] [pn:similarity to uba1p and human ubiquitin-activating enzyme e1-ubiquitin-activating enzyme e1-like:polymerase-interacting protein 2] [gn:uba2:ual1:pip2:d9509] [gtcf:10.1:10.11:10.2:10.9] [keggf:14.2] [sgdfc:4.10.0:6.5]
CONTIG4290	875288_c2_9	4700	18803	777	259	YDR390C	175	2.0(10)-12	Saccharomyces cerevisiae	[ui:ydr390c] [pn:similarity to uba1p and human ubiquitin-activating enzyme e1-ubiquitin-activating enzyme e1-like:polymerase-interacting protein 2] [gn:uba2:ual1:pip2:d9509] [gtcf:10.1:10.11:10.2:10.9] [keggf:14.2] [sgdfc:4.10.0:6.5]
CONTIG2068	4102290_f2_1	4701	18804	828	276	YDR392W	784	5.0(10)-78	Saccharomyces cerevisiae	[ui:ydr392w] [pn:regulatory protein:spt3 protein:positive regulator of ty transcription] [gn:spt3:d9509] [gtcf:10.1:10.2:12.9] [keggf:14.2] [sgdfc:3.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5754	29554682_c3_37	4702	18805	1026	342	YDR432W	237	1.3(10)-19	Saccharomyces cerevisiae	[ui:ydr432w] [pn:nucleolar protein:nucleolar protein 3:mitochondrial targeting suppressor 1 protein] [gn:nop3:npl3:mts1:d9461] [gtcf:10.1:10.2:10.3:10.7:11:12.3] [keggf:14.2] [sgdfc:4.2.0:4.11.0:6.2.0:8.1.0:9.5.0] [db:gtc-saccharom]

CONTIG3941	605208_f2_1	4703	18806	2769	923	YDR443C	119	1.8(10)-12	Saccharomyces cerevisiae	[ui:ydr443c] [pn:dna-directed mna polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit:suppressor of rna polymerase b srb9:scal protein] [gn:srb9:scal:ssn2] [gtcf:10.1:10.2:12.13] [keggfc:14.2] [sgdfe:1.5.2:4.8.1:9]
CONTIG5734	9792001_f1_2	4704	18807	1734	578	YDR443C	262	4.9(10)-19	Saccharomyces cerevisiae	[ui:ydr443c] [pn:dna-directed mna polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit:suppressor of rna polymerase b srb9:scal protein] [gn:srb9:scal:ssn2] [gtcf:10.1:10.2:12.13] [keggfc:14.2] [sgdfe:1.5.2:4.8.1:9]
CONTIG2067	33364063_c3_8	4705	18808	630	210	YDR448W	369	4.7(10)-34	Saccharomyces cerevisiae	[ui:ydr448w] [pn:transcriptional adaptor:potential transcriptional adaptor] [gn:ada2:d9461] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfe:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2067	20507813_c1_6	4706	18809	768	256	YDR448W	803	4.7(10)-80	Saccharomyces cerevisiae	[ui:ydr448w] [pn:transcriptional adaptor:potential transcriptional adaptor] [gn:ada2:d9461] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfe:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3191	4945755_f2_1	4707	18810	1497	499	YEL061C	463	1.8(10)-47	Saccharomyces cerevisiae	[ui:yel061c] [pn:kinesin-related protein:kinesin-like protein cin8] [gn:cin8:ksl2] [gtcf:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfe:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5049	14537503_f2_4	4708	18811	1083	361	YEL037C	297	3.2(10)-35	Saccharomyces cerevisiae	[ui:yel037c] [pn:nucleotide excision repair protein:uv excision repair protein rad23] [gn:rad23:sygp-orf29] [gtcf:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5:0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1546	250700_c1_3	4709	18812	798	266	YEL032W	315	4.0(10)-27	Saccharomyces cerevisiae	[ui:yel032w] [pn:replication initiation protein:minichromosome maintenance protein 3] [gn:mcm3:sygp-orf23] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG2343	10022567_c3_5	4710	18813	186	62	YEL032W	98	0.00062	Saccharomyces cerevisiae	[ui:yel032w] [pn:replication initiation protein:minichromosome maintenance protein 3] [gn:mcm3:sygp-orf23] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG2767	26600302_c1_2	4711	18814	1305	435	YEL032W	1162	1.8(10)-125	Saccharomyces cerevisiae	[ui:yel032w] [pn:replication initiation protein:minichromosome maintenance protein 3] [gn:mcm3:sygp-orf23] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6:0:9.5:0] [db:gtc-saccharomyces cerevisiae]

CONTIG4538	79808_c3_4	4712	18815	945	315	YEL009C	239	2.7(10)-20	Saccharomyces cerevisiae	[ui:ye1009c] [pn:transcriptional activator of amino acid biosynthetic genes:general control protein gcn4:amino acid biosynthesis regulatory protein] [gn:gcn4:arg9:aas3] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:1.1.2.4.8.2:9.5.0] [db:gtc]
CONTIG1851	5175257_c1_2	4713	18816	1176	392	YER013W	346	2.6(10)-30	Saccharomyces cerevisiae	[ui:yer013w] [pn:pre-mrna splicing factor:pre-mrna splicing factor rna helicase] [gn:prp22] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5798	7120932_c3_41	4714	18817	1857	619	YER013W	2018	8.5(10)-209	Saccharomyces cerevisiae	[ui:yer013w] [pn:pre-mrna splicing factor:pre-mrna splicing factor rna helicase] [gn:prp22] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5798	22454051_c2_35	4715	18818	1287	429	YER013W	314	8.3(10)-52	Saccharomyces cerevisiae	[ui:yer013w] [pn:pre-mrna splicing factor:pre-mrna splicing factor rna helicase] [gn:prp22] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4666	2401009_c1_10	4716	18819	558	186	YER013W	248	7.5(10)-20	Saccharomyces cerevisiae	[ui:yer013w] [pn:pre-mrna splicing factor:pre-mrna splicing factor rna helicase] [gn:prp22] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5728	23649056_f2_8	4717	18820	1467	489	YER022W	457	4.5(10)-43	Saccharomyces cerevisiae	[ui.yer022w] [pn:dna-directed ma polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit:suppressor of ma polymerase b] [gn:srb4] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5601	26605093_c2_27	4718	18821	858	286	YER045C	114	1.2(10)-9	Saccharomyces cerevisiae	[ui.yer045c] [pn:weak similarity to transcription factor sko1p:hypothetical 54.6 kd protein in mei4-caj1 intergenic region] [gtcf:10.2] [keggf:14.2] [sgdfc:9.5.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5813	34422150_f3_28	4719	18822	1734	578	YER068W	737	4.7(10)-73	Saccharomyces cerevisiae	[ui.yer068w] [pn:transcriptional repressor:general negative regulator of transcription subunit 4] [gn:not4:mot2:ssf1:sgl1:cc11] [gtcf:10.1:10.2:12.9] [keggf:14.2] [sgdfc:3.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3009	12580327_c2_6	4720	18823	774	258	YER088C	248	3.1(10)-20	Saccharomyces cerevisiae	[ui.yer088c] [pn:weak similarity human transforming proteins:b-myb:hypothetical 73.0 kd protein in seb1-trp2 intergenic region] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3394	10442711_f2_2	4721	18824	651	217	YER095W	866	1.0(10)-86	Saccharomyces cerevisiae	[ui:yer095w] [pn:dna repair protein] [gn:rad51] [gtcf:10.1:10.10:10.2:10.8:12.9] [keggfc:14.2] [sgdfc:3.3.0:3.7.0:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5655	468950_c3_21	4722	18825	1152	384	YER107C	159	2.8(10)-9	Saccharomyces cerevisiae	[ui:yer107c] [pn:required for nuclear pore complex structure and function:hypothetical 40.5 kd protein in nup157-pdh5 intergenic region] [gn:gle2] [gtcf:10.1:10.2:12.3] [keggfc:14.2] [sgdfc:4.1.0:8.1.0:9.2.0:9.5.0] [db:gtc-saccharom]
CONTIG3390	14113300_c1_2	4723	18826	1773	591	YER111C	114	0.00449	Saccharomyces cerevisiae	[ui:yer111c] [pn:transcription factor:regulatory protein swi4:cell-cycle box factor, chain swi4:art1 protein] [gn:swi4:art1] [gtcf:10.1:10.2:12.8] [keggfc:13.1] [sgdfc:3.8.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3587	433332_f2_1	4724	18827	711	237	YER111C	194	4.0(10)-14	Saccharomyces cerevisiae	[ui:yer111c] [pn:transcription factor:regulatory protein swi4:cell-cycle box factor, chain swi4:art1 protein] [gn:swi4:art1] [gtcf:10.1:10.2:12.8] [keggfc:13.1] [sgdfc:3.8.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2567	20319501_f2_3	4725	18828	390	130	YER112W	196	1.0(10)-15	Saccharomyces cerevisiae	[lui:yer112w] [pn:u6 snma-associated protein:u6 snma-associated protein] [gn:uss1:sdb23] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2741	598342_c3_12	4726	18829	1455	485	YER122C	488	5.5(10)-71	Saccharomyces cerevisiae	[lui:yer122c] [pn:zinc finger protein] [gn:gl03] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.8.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5574	7226587_f1_1	4727	18830	951	317	YER142C	398	4.0(10)-37	Saccharomyces cerevisiae	[lui:yer142c] [pn:dna-3-methyladenine glycosidase:3-methyladenine dna glycosylase] [gn:mag1:mag] [gtcf:10.1:10.10:10.2:14.1] [ec:3.2.2.21] [keggf:14.1] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4776	15718812_f3_4	4728	18831	759	253	YER148W	813	4.2(10)-81	Saccharomyces cerevisiae	[lui:yer148w] [pn:tffid and tffib subunit,transcription initiation factor tffid:tata-box factor:tata sequence-binding protein:tp:transcription factor d] [gn:spt15:btf1] [gtcf:10.1:10.2:10.3] [keggf:14.2] [sgdfc:4.1.0:4.4.0:4.8.1:9

CONTIG2031	16485801_f3_4	4729	18832	1038	346	YER161C	163	1.1(10)-11	Saccharomyces cerevisiae	[ui:yer161c] [pn:multifunctional hmg-like chromatin protein:spt2 protein:negative regulator of ty transcription] [gn:spt2:spm2:sin1] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2681	20410150_f1_1	4730	18833	1179	393	YER162C	476	7.0(10)-45	Saccharomyces cerevisiae	[ui:yer162c] [pn:excision repair protein:dna repair protein] [gn:rad4] [gtcf:10.1:10.10:10.2] [keggf:14.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4672	35798416_c3_9	4731	18834	774	258	YER162C	279	1.8(10)-23	Saccharomyces cerevisiae	[ui:yer162c] [pn:excision repair protein:dna repair protein] [gn:rad4] [gtcf:10.1:10.10:10.2] [keggf:14.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4715	9930401_f3_6	4732	18835	894	298	YER165W	574	8.9(10)-56	Saccharomyces cerevisiae	[ui:yer165w] [pn:mrna polyadenylate-binding protein:polyadenylate-binding protein, cytoplasmic and nuclear:pabp:ars consensus binding protein acbp-67:polyadenylate tail-binding protein] [gn:pab1] [gtcf:10.1:10.2:10.7:10.9] [keggf:14

CONTIG479	10975405_f2_1	4733	18836	531	177	YER165W	509	6.9(10)-49	Saccharomyces cerevisiae	[ui:yer165w] [pn:mma polyadenylate-binding protein:polyadenylate-binding protein, cytoplasmic and nuclear:pabp:ars consensus binding protein acbp-67:polyadenylate tail-binding protein] [gn:pab1] [gtcf:10.1:10.2:10.7:10.9] [keggfc:14]
CONTIG4129	30085927_c1_12	4734	18837	2121	707	YER171W	2837	1.3(10)-295	Saccharomyces cerevisiae	[ui:yer171w] [pn:dna helicase/atpase:dna repair helicase rad3] [gn:rad3:rem1] [gtcf:10.1:10.10:10.2] [keggfc:14.2] [sgdgc:4.8.1:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1980	36226442_f2_2_	4735	18838	564	188	YER179W	767	3.1(10)-76	Saccharomyces cerevisiae	[ui:yer179w] [pn:meiosis-specific protein:meiotic recombination protein dmc1] [gn:dmc1:isc2] [gtcf:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdgc:3.5.0:3.7.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG820	6423252_fl_1	4736	18839	711	237	YER184C	98	0.021	Saccharomyces cerevisiae	[ui:yer184c] [pn:similarity to multidrug resistance proteins pdr3p and pdr1p:putative 91.1 kd transcriptional regulatory protein in isc10 3"region] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2763	2736251_fl_1	4737	18840	744	248	YFL031W	230	2.5(10)-19	Saccharomyces cerevisiae	[ui:yfl031w] [pn:transcription factor:hac1 protein] [gn:hac1:ire2] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5803	14488952_c1_20	4738	18841	1416	472	YFL008W	831	1.5(10)-82	Saccharomyces cerevisiae	[ui:yfl008w] [pn:chromosome segregation protein:chromosome segregation protein smc1:da-box protein smc1] [gn:smc1:chl10] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.8.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5803	10656932_c3_33	4739	18842	2379	793	YFL008W	1224	1.2(10)-124	Saccharomyces cerevisiae	[ui:yfl008w] [pn:chromosome segregation protein:chromosome segregation protein smc1:da-box protein smc1] [gn:smc1:chl10] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.8.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5276	14631563_fl_2	4740	18843	2481	827	YFL003C	1155	2.3(10)-117	Saccharomyces cerevisiae	[ui:yfl003c] [pn:meiosis-specific protein:mut protein homolog 4] [gn:msh4] [gtcf:10.1:10.2:10.8:12.8] [keggf:14.2] [sgdfc:3.5.0.3.7.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG413	33406877_c3_5	4741	18844	489	163	YFL002C	344	8.8(10)-31	Saccharomyces cerevisiae	[ui:yfl002c] [pn:atp-dependent rna helicase of deah box family:atp-dependent rna helicase] [gn:spb4] [gtcf:10.1:10.2:10.3] [keggf:14.2] [sgdfc:4.2.0.9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG413	24410682_c3_4	4742	18845	315	105	YFL002C	216	7.2(10)-17	Saccharomyces cerevisiae	[ui:yfl002c] [pn:atp-dependent rna helicase of deah box family:atp-dependent rna helicase] [gn:spb4] [gtfc:10.1:10.2:10.3] [keggc:14.2] [sgdgc:4.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG500	30367268_f1_1	4743	18846	384	128	YFL002C	109	2.2(10)-5	Saccharomyces cerevisiae	[ui:yfl002c] [pn:atp-dependent rna helicase of deah box family:atp-dependent rna helicase] [gn:spb4] [gtfc:10.1:10.2:10.3] [keggc:14.2] [sgdgc:4.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5037	19953762_f2_2	4744	18847	1233	411	YFR002W	367	7.7(10)-33	Saccharomyces cerevisiae	[ui:yfr002w] [pn:nuclear pore protein:96 kd nucleoporin-interacting component] [gn:nic96] [gtfc:10.1:10.2] [keggc:14.2] [sgdgc:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5037	24062751_f3_3	4745	18848	1839	613	YFR002W	608	2.2(10)-59	Saccharomyces cerevisiae	[ui:yfr002w] [pn:nuclear pore protein:96 kd nucleoporin-interacting component] [gn:nic96] [gtfc:10.1:10.2] [keggc:14.2] [sgdgc:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4980	1195277_c1_5	4746	18849	2469	823	YFR031C	1751	1.7(10)-180	Saccharomyces cerevisiae	[ui:yfr031c] [pn:chromosome segregation protein:da-box protein] [gn:smc2] [gtfc:10.1:10.2:12.8] [keggc:14.2] [sgdgc:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5730	22141556_c1_13	4747	18850	903	301	YFR031C	1054	1.2(10)-106	Saccharomyces cerevisiae	[ui:yfr031c] [pn:chromosome segregation protein:da-box protein] [gn:smc2] [gtcf:10.1:10.2:12.8] [keggc:14.2] [sgdfe:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3742	13846061_c1_7	4748	18851	711	237	YFR034C	109	0.00023	Saccharomyces cerevisiae	[ui:yfr034c] [pn:transcription factor:phosphate system positive regulatory protein] [gn:pho4] [gtcf:10.1:10.2:12.8:13.10] [keggc:13.2] [sgdfe:1.4.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1011	26172255_c2_3	4749	18852	840	280	YGL251C	443	9.0(10)-41	Saccharomyces cerevisiae	[ui:ygl251c] [pn:dna/ma helicase:hfm1 protein] [gn:hfm1:nre1046] [gtcf:10.1:10.2] [keggc:14.2] [sgdfe:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5468	26223519_c1_13	4750	18853	906	302	YGL251C	170	8.3(10)-10	Saccharomyces cerevisiae	[ui:ygl251c] [pn:dna/ma helicase:hfm1 protein] [gn:hfm1:nre1046] [gtcf:10.1:10.2] [keggc:14.2] [sgdfe:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
b3x11387.y	26188424_c1_4	4751	18854	594	198	YGL251C	441	1.5(10)-40	Saccharomyces cerevisiae	[ui:ygl251c] [pn:dna/ma helicase:hfm1 protein] [gn:hfm1:nre1046] [gtcf:10.1:10.2] [keggc:14.2] [sgdfe:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2495	4119381_f3_1	4752	18855	1392	464	YGL238W	515	1.2(10)-48	Saccharomyces cerevisiae	[ui:ygl238w] [pn:probable kinetochore protein:chromosome segregation protein] [gn:cse1] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8.0:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4965	25428812_c2_7	4753	18856	192	64	YGL238W	161	1.2(10)-10	Saccharomyces cerevisiae	[ui:ygl238w] [pn:probable kinetochore protein:chromosome segregation protein] [gn:cse1] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8.0:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
b9x13e15.y	14896887_f1_1	4754	18857	906	302	YGL238W	641	1.8(10)-62	Saccharomyces cerevisiae	[ui:ygl238w] [pn:probable kinetochore protein:chromosome segregation protein] [gn:cse1] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8.0:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2187	39511_f3_3	4755	18858	642	214	YGL237C	195	1.3(10)-15	Saccharomyces cerevisiae	[ui:ygl237c] [pn:ccaat-binding factor subunit:transcriptional activator] [gn:hap2] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2563	14882907_f3_2	4756	18859	840	280	YGL237C	279	1.6(10)-24	Saccharomyces cerevisiae	[ui:ygl237c] [pn:ccaat-binding factor subunit:transcriptional activator] [gn:hap2] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2845	23595207_c3_4	4757	18860	1605	535	YGL208W	185	1.1(10)-11	Saccharomyces cerevisiae	[ui:ygl208w] [pn:dominant suppressor of some ts mutations in rpo21 and prp4:sip2 protein:spm2 protein] [gn:sip2:spm2] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfe:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4654	24410451_f3_8	4758	18861	1182	394	YGL207W	611	6.5(10)-59	Saccharomyces cerevisiae	[ui:ygl207w] [pn:general chromatin factor:cell division control protein 68] [gn:cdc68:spt16:ssf1] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfe:3.8.0:4.8.3:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4654	9978176_f1_3	4759	18862	1350	450	YGL207W	1013	2.7(10)-102	Saccharomyces cerevisiae	[ui:ygl207w] [pn:general chromatin factor:cell division control protein 68] [gn:cdc68:spt16:ssf1] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfe:3.8.0:4.8.3:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4654	1993950_f2_6	4760	18863	291	97	YGL207W	327	2.3(10)-28	Saccharomyces cerevisiae	[ui:ygl207w] [pn:general chromatin factor:cell division control protein 68] [gn:cdc68:spt16:ssf1] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfe:3.8.0:4.8.3:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG563	12207031_c3_5	4761	18864	234	78	YGL207W	209	9.5(10)-16	Saccharomyces cerevisiae	[ui:ygl207w] [pn:general chromatin factor:cell division control protein 68] [gn:cdc68:spt16:ssf1] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdgc:3.8.0.4.8.3:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5011	5120427_c3_11	4762	18865	1638	546	YGL192W	1023	2.2(10)-103	Saccharomyces cerevisiae	[ui:ygl192w] [pn:positive transcription factor for ime2:transcriptional regulator spo8] [gn:spo8:ime4:g1337] [gtcf:10.1:10.2:12.15] [keggf:14.2] [sgdgc:3.4.0.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4386	12000402_f1_1	4763	18866	1023	341	YGL172W	221	1.0(10)-26	Saccharomyces cerevisiae	[ui:ygl172w] [pn:nuclear pore protein:nucleoporin nup49/nsp49:nuclear pore protein nup49/nsp49] [gn:nup49:nsp49:g1648] [gtcf:10.1:10.2:12.3] [keggf:14.2] [sgdgc:4.11.0.8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
b9x10w60.x	29847157_f1_1	4764	18867	528	176	YGL172W	101	0.00012	Saccharomyces cerevisiae	[ui:ygl172w] [pn:nuclear pore protein:nucleoporin nup49/nsp49:nuclear pore protein nup49/nsp49] [gn:nup49:nsp49:g1648] [gtcf:10.1:10.2:12.3] [keggf:14.2] [sgdgc:4.11.0.8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3057	12782292_f3_2	4765	18868	1212	404	YGL166W	118	5.9(10)-5	Saccharomyces cerevisiae	[ui:ygl166w] [pn:copper-dependent transcription factor:transcriptional activator protein ace1:copper- first transcription factor] [gn:ace1:cup2:g1810] [gtcf:10.1:10.2:12.6] [keggfc:14.2] [sgdfc:1.8.1:4.8.2:9.5.0] [db:gtc-saccharomyces]
CONTIG1666	480126_f1_1	4766	18869	816	272	YGL163C	1014	2.1(10)-102	Saccharomyces cerevisiae	[ui:ygl163c] [pn:dna-dependent atpase of the snf2p family:dna repair and recombination protein rad54] [gn:rad54:g1821] [gtcf:10.1:10.10:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.7.0:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2995	11723211_c2_8	4767	18870	1257	419	YGL163C	486	3.8(10)-82	Saccharomyces cerevisiae	[ui:ygl163c] [pn:dna-dependent atpase of the snf2p family:dna repair and recombination protein rad54] [gn:rad54:g1821] [gtcf:10.1:10.10:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.7.0:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
b3x16060.y	35838517_f3_1	4768	18871	378	126	YGL163C	129	2.7(10)-7	Saccharomyces cerevisiae	[ui:ygl163c] [pn:dna-dependent atpase of the snf2p family:dna repair and recombination protein rad54] [gn:rad54:g1821] [gtcf:10.1:10.10:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5.0:3.7.0:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG2515	25509687_c3_3	4769	18872	762	254	YGL115W	763	8.3(10)-76	Saccharomyces cerevisiae	[ui:ygl115w] [pn:nuclear regulatory protein:nuclear protein snf4:regulatory protein cat3] [gn:snf4:cat3] [gtcf:10.1:10.2:12.13:13.2] [keggfc:14.2] [sgdfc:1.5.2:4.8.2:9.5.0:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2496	33754007_c1_5	4770	18873	906	302	YGL112C	653	3.7(10)-64	Saccharomyces cerevisiae	[ui:ygl112c] [pn:tfiid subunit:tbp-associated protein complex, tfiid 60 kd subunit:tafi-60] [gn:taf60:g2985] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4476	31921888_f1_1	4771	18874	528	176	YGL112C	95	0.01099	Saccharomyces cerevisiae	[ui:ygl112c] [pn:tfiid subunit:tbp-associated protein complex, tfiid 60 kd subunit:tafi-60] [gn:taf60:g2985] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5761	33207500_c1_18	4772	18875	1140	380	YGL100W	735	9.0(10)-94	Saccharomyces cerevisiae	[ui:ygl100w] [pn:nuclear pore protein] [gn:seh1] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1734	15664163_f2_1	4773	18876	462	154	YGL097W	479	1.0(10)-45	Saccharomyces cerevisiae	[ui:ygl097w] [pn:gdp/gtp exchange factor for gsp1p/gsp2p:regulator of chromosome condensation:prp20 protein:pheromone response pathway component srm1] [gn:prp20:srm1:mtr1] [gtcf:10.1:10.2:10.3:10.6:10.9:12.3:12.8:12.9] [keggfc:13.3]
CONTIG4261	16853436_c3_6	4774	18877	1014	338	YGL097W	839	7.4(10)-84	Saccharomyces cerevisiae	[ui:ygl097w] [pn:gdp/gtp exchange factor for gsp1p/gsp2p:regulator of chromosome condensation:prp20 protein:pheromone response pathway component srm1] [gn:prp20:srm1:mtr1] [gtcf:10.1:10.2:10.3:10.6:10.9:12.3:12.8:12.9] [keggfc:13.3]
CONTIG4989	5254555_c3_7	4775	18878	1215	405	YGL097W	109	5.2(10)-5	Saccharomyces cerevisiae	[ui:ygl097w] [pn:gdp/gtp exchange factor for gsp1p/gsp2p:regulator of chromosome condensation:prp20 protein:pheromone response pathway component srm1] [gn:prp20:srm1:mtr1] [gtcf:10.1:10.2:10.3:10.6:10.9:12.3:12.8:12.9] [keggfc:13.3]

CONTIG5116	14885931_c1_6	4776	18879	1464	488	YGL097W	134	1.0(10)-5	Saccharomyces cerevisiae	[ui:ygl097w] [pn:gdp/gtp exchange factor for gsp1p/gsp2p:regulator of chromosome condensation:prp20 protein:pheromone response pathway component srm1] [gn:prp20-srm1-mtr1] [gtcf:10.1:10.2:10.3:10.6:10.9:12.3:12.8:12.9] [keggfc:13.3]
CONTIG1557	24788942_f1_1	4777	18880	942	314	YGL092W	111	4.5(10)-7	Saccharomyces cerevisiae	[ui:ygl092w] [pn:nucleoporin:nuclear pore protein] [gn:nup145] [gtcf:10.1:10.2:10.6:12.3] [keggfc:14.2] [sgdgc:4.5:0:4.11:0:8.1:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG2555	23524192_c3_3	4778	18881	1656	552	YGL092W	231	1.3(10)-15	Saccharomyces cerevisiae	[ui:ygl092w] [pn:nucleoporin:nuclear pore protein] [gn:nup145] [gtcf:10.1:10.2:10.6:12.3] [keggfc:14.2] [sgdgc:4.5:0:4.11:0:8.1:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG2189	19734676_f1_2	4779	18882	1194	398	YGL086W	121	0.00029	Saccharomyces cerevisiae	[ui:ygl086w] [pn:spindle assembly checkpoint protein:spindle assembly protein] [gn:mad1] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8:0:9.5:0] [db:gtc-saccharomyces cerevisiae]

CONTIG2444	4806436_c2_3	4780	18883	1923	641	YGL086W	346	1.2(10)-28	Saccharomyces cerevisiae	[ui:ygl086w] [pn:spindle assembly checkpoint protein:spindle assembly checkpoint component:mitotic protein] [gn:mad1] [gicf:10.1:10.2:12.8] [keggf:14.2] [sgdfe:3.8.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5431	26692299_c1_9	4781	18884	960	320	YGL078C	1095	5.5(10)-111	Saccharomyces cerevisiae	[ui:ygl078c] [pn:putative ma helicase required for pre-rna processing:probable atp-dependent rna helicase ca3] [gn:dbp3] [gicf:10.1:10.2:10.3] [keggf:14.2] [sgdfe:4.2.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5275	33407202_c1_17	4782	18885	915	305	YGL071W	95	6.5(10)-6	Saccharomyces cerevisiae	[ui:ygl071w] [pn:iron-regulated transcriptional repressor:iron-regulated transcriptional repressor aft1] [gn:aft1:rcs1] [gicf:10.1:10.2:12.6] [keggf:14.2] [sgdfe:1.8.1:4.8.2:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG4253	12611055_c3_8	4783	18886	411	137	YGL058W	483	3.8(10)-46	Saccharomyces cerevisiae	[ui:ygl058w] [pn:ubiquitin conjugating enzyme:ubiquitin-conjugating enzyme e2-20 kd:ubiquitin- protein ligase:ubiquitin carrier protein] [gn:ubc2:rad6] [gicf:10.1:10.10:10.2:10.7:10.8:12.15:14.1] [ec:6.3.2.19] [keggf:14.1] [sgdfe:3.

CONTIG4173	9801537_c2_9	4784	18887	1122	374	YGL044C	112	0.00052	Saccharomyces cerevisiae	[ui:ygl044c] [pn:component of pre-mrna 3'-end processing factor cf i:mma 3'-end processing protein] [gn:ma15] [gtcf:10.1:10.2:10.9] [keggf:14.2] [sgdfc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5749	20742187_c2_22	4785	18888	837	279	YGL044C	218	4.7(10)-18	Saccharomyces cerevisiae	[ui:ygl044c] [pn:component of pre-mrna 3'-end processing factor cf i:mma 3'-end processing protein] [gn:ma15] [gtcf:10.1:10.2:10.9] [keggf:14.2] [sgdfc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5749	19615635_f3_10	4786	18889	939	313	YGL043W	455	5.5(10)-63	Saccharomyces cerevisiae	[ui:ygl043w] [pn:tfiis:transcription elongation factor:transcription elongation factor s-ii:dna strand transfer protein alpha:stp-alpha:dna strand transferase 1:pyrimidine pathway regulatory protein 2] [gn:dst1:ppr2] [gtcf:10.1:10.2:1
CONTIG1873	785627_fl_3	4787	18890	753	251	YGL035C	241	9.1(10)-20	Saccharomyces cerevisiae	[ui:ygl035c] [pn:transcriptional repressor:regulatory protein mig1:regulatory protein cat4] [gn:mig1:cat4:ssn1] [gtcf:10.1:10.2:12.13] [keggf:14.2] [sgdfc:1.5.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2619	783132_c3_9	4788	18891	1527	509	YGL035C	241	1.3(10)-18	Saccharomyces cerevisiae	[ui:ygl035c] [pn:transcriptional repressor:regulatory protein mig1:regulatory protein cat4] [gn:mig1:cat4:ssn1] [gtcf:10.1:10.2:12.13] [keggfc:14.2] [sgdfc:1.5.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5297	24407812_f2_7	4789	18892	528	176	YGL035C	273	2.7(10)-23	Saccharomyces cerevisiae	[ui:ygl035c] [pn:transcriptional repressor:regulatory protein mig1:regulatory protein cat4] [gn:mig1:cat4:ssn1] [gtcf:10.1:10.2:12.13] [keggfc:14.2] [sgdfc:1.5.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5245	15630261_c3_23	4790	18893	909	303	YGL019W	667	1.2(10)-65	Saccharomyces cerevisiae	[ui:ygl019w] [pn:casein kinase ii, beta subunit:casein kinase ii beta chain:ck ii] [gn:ckb1] [gtcf:10.1:10.2:12.13:14.1] [ec:2.7.1.37] [keggfc:14.1] [sgdfc:4.0:9.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3649	260_c2_7	4791	18894	696	232	YGL013C	113	0.00027	Saccharomyces cerevisiae	[ui:ygl013c] [pn:transcription factor:pleiotropic drug resistance regulatory protein 1] [gn:pdr1:ant1:bor2:cyh3:nra2:smr2] [gtcf:10.1:10.2:12.12] [keggfc:14.2] [sgdfc:4.8.2:9.5.0:11.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4336	476550_c1_7	4792	18895	564	188	YGL013C	117	6.5(10)-6	Saccharomyces cerevisiae	[ui:ygl013c] [pn:transcription factor:pleiotropic drug resistance regulatory protein 1] [gn:pdrl:ant1:bor2:cyh3:nra2:smr2] [gtcf:10.1:10.2:12.12] [keggc:14.2] [sgdfc:4.8.2:9.5.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1472	4797027_f1_1	4793	18896	909	303	YGR005C	325	2.2(10)-29	Saccharomyces cerevisiae	[ui:ygr005c] [pn:tfiif subunit:transcription initiation factor, 54 kd:transcription initiation factor iif, beta subunit:tfiif- beta:tfiif medium subunit:transcription factor g 54 kd subunit] [gn:tfg2] [gtcf:10.1:10.2] [keggc:14.2] [
CONTIG1981	5875001_f2_2	4794	18897	684	228	YGR006W	123	4.5(10)-6	Saccharomyces cerevisiae	[ui:ygr006w] [pn:u5 snrna-associated protein:pre-mrna splicing factor] [gn:prp18] [gtcf:10.1:10.2] [keggc:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3978	35332807_f1_1	4795	18898	1218	406	YGR044C	154	1.3(10)-8	Saccharomyces cerevisiae	[ui:ygr044c] [pn:zinc-finger transcription factor:zinc finger protein] [gn:rme1] [gtcf:10.1:10.2:12.8] [keggc:13.1] [sgdfc:3.5.0:3.8.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5713	13706525_c3_21	4796	18899	351	117	YGR063C	259	2.1(10)-22	Saccharomyces cerevisiae	[ui:ygr063c] [pn:transcription initiation protein] [gn:spi4] [gtcf:10.1:10.2:10.8] [keggc:14.2] [sgdfc:3.7.0:4.8.1:4.8.3:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5447	22054035_c1_13	4797	18900	366	122	YGR074W	100	1.5(10)-5	Saccharomyces cerevisiae	[ui:ygr074w] [pn:snrna-associated protein:small nuclear ribonucleoprotein d1 homolog] [gn:smd1] [gtcf:10.1:10.2:12.16] [keggfc:14.2] [sgdfc:4.9.0:6.4.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1368	25502175_f2_1	4798	18901	942	314	YGR091W	345	1.5(10)-35	Saccharomyces cerevisiae	[ui:ygr091w] [pn:pre-mrna splicing protein:pre-mrna splicing factor] [gn:prp31] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3144	448957_f1_1	4799	18902	2007	669	YGR098C	237	5.2(10)-16	Saccharomyces cerevisiae	[ui:ygr098c] [pn:required for normal spindle structure:protein] [gn:esp1] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG582	4695411_c1_3	4800	18903	735	245	YGR098C	255	2.2(10)-20	Saccharomyces cerevisiae	[ui:ygr098c] [pn:required for normal spindle structure:protein] [gn:esp1] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4432	6407830_f3_8	4801	18904	753	251	YGR099W	144	1.1(10)-7	Saccharomyces cerevisiae	[ui:ygr099w] [pn:involved in controlling telomere length and position effect:telomere length regulation protein] [gn:tel2] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4432	21666581_fl_1	4802	18905	585	195	YGR099W	103	0.00489	Saccharomyces cerevisiae	[ui:YGR099W] [pn:involved in controlling telomere length and position effect:telomere length regulation protein] [gn:tel2] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5789	6855033_c3_30	4803	18906	897	299	YGR104C	143	8.9(10)-13	Saccharomyces cerevisiae	[ui:YGR104C] [pn:dna-directed rna polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit:suppressor of rna polymerase b] [gn:srb5] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG801	26750450_c3_3	4804	18907	1119	373	YGR116W	501	1.1(10)-46	Saccharomyces cerevisiae	[ui:YGR116W] [pn:transcription initiation protein:transcription initiation protein spt6] [gn:spt6:ssn20:cre2:g6169] [gtcf:10.1:10.2:10.8] [keggf:14.2] [sgdf:3.7.0:4.8.1:4.8.3:9.5.0] [db:gtc-saccharomyces cerevisiae]
b2x10868.y	10828302_fl_1	4805	18908	522	174	YGR116W	203	6.5(10)-15	Saccharomyces cerevisiae	[ui:YGR116W] [pn:transcription initiation protein:transcription initiation protein spt6] [gn:spt6:ssn20:cre2:g6169] [gtcf:10.1:10.2:10.8] [keggf:14.2] [sgdf:3.7.0:4.8.1:4.8.3:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG892	10347312_fl_1	4806	18909	606	202	YGR119C	192	2.2(10)-14	Saccharomyces cerevisiae	[ui:ygr119c] [pn:nuclear pore protein:nucleoporin nup57:nuclear pore protein nup57] [gn:nup57:g6320] [gtcf:10.1:10.2] [keggc:14.2] [sgdgc:8.1.0-9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5795	16829705_c3_42	4807	18910	1209	403	YGR159C	698	6.4(10)-69	Saccharomyces cerevisiae	[ui:ygr159c] [pn:nuclear localization sequence binding protein:p67] [gn:nsr1:g7001] [gtcf:10.1:10.2:10.3:13.2] [keggc:14.2] [sgdgc:4.2.0-9.5.0:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4405	15019625_fl_1	4808	18911	1635	545	YGR186W	387	2.5(10)-56	Saccharomyces cerevisiae	[ui:ygr186w] [pn:tfiif subunit:transcription initiation factor, 105 kd:transcription initiation factor iif, alpha subunit:tfiif-alpha:tfiif large subunit:transcription factor g 105 kd subunit:p105] [gn:tfgl:ssu71:g7526] [gtcf:10.1:10.
CONTIG1831	819637_c3_4	4809	18912	633	211	YGR229C	131	5.4(10)-7	Saccharomyces cerevisiae	[ui:ygr229c] [pn:beta-1,3-glucan synthesis protein:smi1 protein:killer toxin resistant protein 4] [gn:smi1:knr4:ktr4:g8553] [gtcf:10.1:10.2:12.13] [keggc:14.2] [sgdgc:1.5.2-9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3039	33250311_c1_3	4810	18913	1296	432	YGR229C	306	6.0(10)-27	Saccharomyces cerevisiae	[ui:ygr229c] [pn:beta-1,3-glucan synthesis protein:smi1 protein:killer toxin resistant protein 4] [gn:smi1:knr4:ptr4:g8553] [gicfc:10.1:10.2:12.13] [keggfc:14.2] [sgdgc:1.5.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3039	2907182_c3_4	4811	18914	426	142	YGR229C	106	3.7(10)-5	Saccharomyces cerevisiae	[ui:ygr229c] [pn:beta-1,3-glucan synthesis protein:smi1 protein:killer toxin resistant protein 4] [gn:smi1:knr4:ptr4:g8553] [gicfc:10.1:10.2:12.13] [keggfc:14.2] [sgdgc:1.5.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3774	24432937_f1_2	4812	18915	693	231	YGR229C	244	4.2(10)-20	Saccharomyces cerevisiae	[ui:ygr229c] [pn:beta-1,3-glucan synthesis protein:smi1 protein:killer toxin resistant protein 4] [gn:smi1:knr4:ptr4:g8553] [gicfc:10.1:10.2:12.13] [keggfc:14.2] [sgdgc:1.5.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4159	23829656_f3_2	4813	18916	1083	361	YGR252W	1398	4.2(10)-143	Saccharomyces cerevisiae	[ui:ygr252w] [pn:histone acetyltransferase:transcriptional activator gcn5] [gn:gcn5:ada4] [gicfc:10.1:10.2:10.7] [keggfc:14.2] [sgdgc:4.8.2:4.8.3:6.3:0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG360	10757661_f1_1	4814	18917	948	316	YGR258C	104	0.024	Saccharomyces cerevisiae	[ui:ygr258c] [pn:structure-specific nuclease of the nucleotide excision repairsome:dna repair protein] [gn:rad2] [gtcf:10.1:10.10:10.2:12.8] [keggfc:14.2] [sgdfc:3.5.0:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5692	6812900_f1_3	4815	18918	447	149	YGR258C	448	2.5(10)-41	Saccharomyces cerevisiae	[ui:ygr258c] [pn:structure-specific nuclease of the nucleotide excision repairsome:dna repair protein] [gn:rad2] [gtcf:10.1:10.10:10.2:12.8] [keggfc:14.2] [sgdfc:3.5.0:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5692	21660937_f2_5	4816	18919	2385	795	YGR258C	647	4.2(10)-103	Saccharomyces cerevisiae	[ui:ygr258c] [pn:structure-specific nuclease of the nucleotide excision repairsome:dna repair protein] [gn:rad2] [gtcf:10.1:10.10:10.2:12.8] [keggfc:14.2] [sgdfc:3.5.0:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1591	24429567_f2_1	4817	18920	1089	363	YGR274C	241	2.0(10)-29	Saccharomyces cerevisiae	[ui:ygr274c] [pn:tfiid subunit:ibp-associated factor, 145 kd:transcription initiation factor tfiid 145 kd subunit:ibp- associated factor 145 kd:tafi-145:tafi-130] [gn:taf145] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.1:4.8.3:9.5.0:

CONTIG3332	35433287_f2_1	4818	18921	564	188	YGR274C	167	3.0(10)-11	Saccharomyces cerevisiae	[ui:ygr274c] [pn:tfid subunit:tbp-associated factor, 145 kd:transcription initiation factor tfid 145 kd subunit:tbp- associated factor 145 kd:tafi-145:tafi-130] [gn:tafi145] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:4.8.1:4.8.3:9.5.0:
b3x13754.x	196075_c3_5	4819	18922	528	176	YGR285C	320	7.2(10)-29	Saccharomyces cerevisiae	[ui:ygr285c] [pn:zuotin, a putative z-dna binding protein:zuotin] [gn:zuol] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5554	1406325_c3_21	4820	18923	615	205	YGR288W	134	3.2(10)-8	Saccharomyces cerevisiae	[ui:ygr288w] [pn:maltose pathway regulatory protein:maltose fermentation regulatory protein mal1r] [gn:mal1r-mal13:g9591] [gtcf:10.1:10.2:12.13] [keggf:14.2] [sgdf:1.5.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4046	10972175_c3_8	4821	18924	855	285	YHL034C	116	6.0(10)-5	Saccharomyces cerevisiae	[ui:yhl034c] [pn:single-strand nucleic acid binding protein:single-stranded nucleic acid-binding protein] [gn:ssb1:ssb1:ssb1] [gtcf:10.1:10.2:10.3] [keggf:14.2] [sgdf:4.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3312	24298461_f2_4	4822	18925	342	114	YHL027W	92	0.0016	Saccharomyces cerevisiae	[ui:yhl027w] [pn:meiotic regulatory protein] [gn:rim101] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.5.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3535	19728432_f1_1	4823	18926	1062	354	YHL027W	358	2.8(10)-32	Saccharomyces cerevisiae	[ui:yhl027w] [pn:meiotic regulatory protein] [gn:rim101] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.5.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3064	33985001_f2_3	4824	18927	993	331	YHL022C	139	8.5(10)-7	Saccharomyces cerevisiae	[ui:yhl022c] [pn:meiosis specific protein] [gn:spo11] [gtcf:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdgc:3.5.0:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5717	10939550_f3_3	4825	18928	624	208	YHR041C	146	7.2(10)-10	Saccharomyces cerevisiae	[ui:yhr041c] [pn:dna-directed rna polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit:suppressor of rna polymerase b] [gn:srb2] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5621	975077_f1_2	4826	18929	453	151	YHR089C	286	2.8(10)-25	Saccharomyces cerevisiae	[ui:yhr089c] [pn:nucleolar rna processing protein:protein] [gn:gar1] [gtcf:10.1:10.2:10.3] [keggfc:14.2] [sgdgc:4.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1193	10315750_c2_9	4827	18930	567	189	YHR118C	104	0.0002	Saccharomyces cerevisiae	[ui:yhr118c] [pn:origin recognition complex, 50 kd subunit:origin recognition complex protein, subunit 6:origin recognition complex protein 50 kd subunit:acs associated protein 1] [gn:orc6:aap1] [gtcf:10.1:10.2:10.8:12.8:12.9] [keggf]
CONTIG5259	14472916_f2_1	4828	18931	2652	884	YHR119W	715	8.5(10)-105	Saccharomyces cerevisiae	[ui:yhr119w] [pn:regulatory protein:hypothetical 123.9 kd protein in orc6-msh1 intergenic region] [gn:ytx1] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8:3.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5721	5864036_c2_23	4829	18932	258	86	YHR129C	178	3.5(10)-13	Saccharomyces cerevisiae	[ui:yhr129c] [pn:contractin:actin-like protein] [gn:act5:act3] [gtcf:10.1:10.2:12.16:12.8] [keggf:14.2] [sgdfc:3.8:0.9:3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3192	4687927_c3_6	4830	18933	660	220	YHR164C	368	1.8(10)-32	Saccharomyces cerevisiae	[ui:yhr164c] [pn:dna helicase:dna replication helicase] [gn:dna2] [gtcf:10.1:10.2:10.8] [keggf:14.2] [sgdfc:3.6:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
b2x10687.x	10829568_f1_1	4831	18934	765	255	YHR164C	231	7.2(10)-18	Saccharomyces cerevisiae	[ui:yhr164c] [pn:dna helicase:dna replication helicase] [gn:dna2] [gtcf:10.1:10.2:10.8] [keggf:14.2] [sgdfc:3.6:0.9:5.0] [db:gtc-saccharomyces cerevisiae]

b2x12186.x	444801_f3_1	4832	18935	519	173	YHR164C	240	7.9(10)-19	Saccharomyces cerevisiae	[lui:yhr164c] [pn:dna helicase:dna replication helicase] [gn:dna2] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
b3x15670.y	12756438_f2_1	4833	18936	486	162	YHR164C	255	2.8(10)-25	Saccharomyces cerevisiae	[lui:yhr164c] [pn:dna helicase:dna replication helicase] [gn:dna2] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1677	433332_f2_1	4834	18937	1128	376	YHR165C	723	6.2(10)-70	Saccharomyces cerevisiae	[lui:yhr165c] [pn:u5 snmp protein, pre-mrna splicing factor:pre-mrna splicing factor prp8] [gn:prp8:ma8:dbf3:dna39] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1685	21521891_c1_5	4835	18938	846	282	YHR165C	895	3.1(10)-88	Saccharomyces cerevisiae	[lui:yhr165c] [pn:u5 snmp protein, pre-mrna splicing factor:pre-mrna splicing factor prp8] [gn:prp8:ma8:dbf3:dna39] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG606	5900312_f3_2	4836	18939	1254	418	YHR165C	1602	7.5(10)-164	Saccharomyces cerevisiae	[lui:yhr165c] [pn:u5 snmp protein, pre-mrna splicing factor:pre-mrna splicing factor prp8] [gn:prp8:ma8:dbf3:dna39] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

b9x13c15.x	4428442_c3_3	4837	18940	201	67	YHR166C	131	1.1(10)-7	Saccharomyces cerevisiae	[ui:yhr166c] [pn:subunit of anaphase-promoting complex:cyclosome:cell division control protein 23] [gn:cdc23] [gtcf:10.1:10.11:10.2:12.16:12.8] [keggfc:13.3] [sgdfc:3.8:0.6:5.1:9.3:0:9:5.0] [db:gtc-saccharomyces cerevisiae]
b9x13c15.x	2917251_c2_2	4838	18941	477	159	YHR166C	523	2.2(10)-50	Saccharomyces cerevisiae	[ui:yhr166c] [pn:subunit of anaphase-promoting complex:cyclosome:cell division control protein 23] [gn:cdc23] [gtcf:10.1:10.11:10.2:12.16:12.8] [keggfc:13.3] [sgdfc:3.8:0.6:5.1:9.3:0:9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG549	1978285_f3_1	4839	18942	516	172	YHR193C	338	9.0(10)-31	Saccharomyces cerevisiae	[ui:yhr193c] [pn:similarity to human alpha-nac:protein] [gn:egd2] [gtcf:10.1:10.2:12.13] [keggfc:14.2] [sgdfc:1.5:2.4:8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4001	12683582_c2_12	4840	18943	240	80	YHR206W	221	2.2(10)-17	Saccharomyces cerevisiae	[ui:yhr206w] [pn:transcription factor with similarity to hsf1p:putative transcription factor skn7:pos9 protein] [gn:skn7:pos9] [gtcf:10.1:10.2:12.8:13.2] [keggfc:14.2] [sgdfc:3.1:0:3.8:0:4.8:2:9:5.0:11.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4001	34563212_c3_15	4841	18944	948	316	YHR206W	184	1.8(10)-19	Saccharomyces cerevisiae	[ui:yhr206w] [pn:transcription factor with similarity to hsf1p:putative transcription factor skn7:pos9] [gn:skn7:pos9] [gtcf:10.1:10.2:12.8:13.2] [keggfc:14.2] [sgdfc:3.1.0:3.8.0:4.8.2:9.5.0:11.1.1.0] [db:gtc-saccharomyces cere]
CONTIG3462	860077_f3_7	4842	18945	477	159	YHR206W	383	4.7(10)-35	Saccharomyces cerevisiae	[ui:yhr206w] [pn:transcription factor with similarity to hsf1p:putative transcription factor skn7:pos9] [gn:skn7:pos9] [gtcf:10.1:10.2:12.8:13.2] [keggfc:14.2] [sgdfc:3.1.0:3.8.0:4.8.2:9.5.0:11.1.1.0] [db:gtc-saccharomyces cere]
CONTIG1455	4490885_c3_6	4843	18946	942	314	YIL143C	1435	5.0(10)-147	Saccharomyces cerevisiae	[ui:yil143c] [pn:dna helicase:dna repair helicase rad25] [gn:rad25:ssl2:uvs112] [gtcf:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:4.8.1:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2685	15792336_c1_5	4844	18947	708	236	YIL143C	823	3.7(10)-82	Saccharomyces cerevisiae	[ui:yil143c] [pn:dna helicase:dna repair helicase rad25] [gn:rad25:ssl2:uvs112] [gtcf:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:4.8.1:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5706	10970255_c1_19	4845	18948	831	277	YIL143C	714	1.3(10)-70	Saccharomyces cerevisiae	[ui:yil143c] [pn:dna helicase:dna repair helicase rad25] [gn:rad25:ssl2:uvr112] [gtcf:10.1:10.10:10.2] [keggfc:14.2] [sgdfe:4.8.1:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1299	20597211_f3_3	4846	18949	1272	424	YIL126W	588	4.9(10)-56	Saccharomyces cerevisiae	[ui:yil126w] [pn:subunit of the rsc complex:nuclear protein sth1/nps1] [gn:sth1:nps1] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfe:3.8.0:4.8.2:4.8.3:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3504	39756_f1_1	4847	18950	1722	574	YIL126W	1555	1.7(10)-169	Saccharomyces cerevisiae	[ui:yil126w] [pn:subunit of the rsc complex:nuclear protein sth1/nps1] [gn:sth1:nps1] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfe:3.8.0:4.8.2:4.8.3:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4330	16453251_c2_6	4848	18951	1254	418	YIL115C	218	2.0(10)-14	Saccharomyces cerevisiae	[ui:yil115c] [pn:nuclear pore protein:nucleoporin nup159:nuclear pore protein nup159] [gn:nup159:rat7] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfe:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3472	22050877_c3_6	4849	18952	786	262	YIL061C	193	2.3(10)-15	Saccharomyces cerevisiae	[ui:yil061c] [pn:u1 small nuclear ribonucleoprotein:u1 small nuclear ribonucleoprotein 70 kd homolog] [gn:snr1] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1816	25433132_c1_3	4850	18953	1119	373	YIL046W	718	1.2(10)-83	Saccharomyces cerevisiae	[ui:yil046w] [pn:involved in regulation of sulfur assimilation genes:protein] [gn:met30] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:1.1.2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4732	23944625_c1_12	4851	18954	1149	383	YIL038C	214	2.0(10)-16	Saccharomyces cerevisiae	[ui:yil038c] [pn:general negative regulator of transcription, subunit 3:general negative regulator of transcription subunit 3] [gn:not3:cdc39] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5775	26370317_c2_27	4852	18955	2334	778	YIL038C	94	1.1(10)-15	Saccharomyces cerevisiae	[ui:yil038c] [pn:general negative regulator of transcription, subunit 3:general negative regulator of transcription subunit 3] [gn:not3:cdc39] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4311	4431966_f3_4	4853	18956	633	211	YIL035C	777	2.7(10)-77	Saccharomyces cerevisiae	[ui:yil035c] [pn:casein kinase ii, catalytic alpha chain:casein kinase ii, alpha chain:ck ii] [gn:cka1] [gtcf:10.1:10.2:12.13:12.8] [ec:2.7.1.37] [keggf:14.1] [sgdfc:3.8.0:4.7.0:9.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3781	2735001_f3_1	4854	18957	1491	497	YJL194W	240	6.2(10)-31	Saccharomyces cerevisiae	[ui:yj1194w] [pn:cell division control protein 6] [gn:cdc6:j0347] [gtcf:10.1:10.2:10.8:12.8] [keggfc:13.2] [sgdfc:3.6:0.3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG20	25587825_c3_1	4855	18958	561	187	YJL176C	218	7.5(10)-17	Saccharomyces cerevisiae	[ui:yj1176c] [pn:transcription regulatory protein:transcription regulatory protein swi3:swi/snf complex component swi3:transcription factor tye2] [gn:swi3:tye2:j0495] [gtcf:10.1:10.2:12.13:12.9] [keggfc:14.2] [sgdfc:1.5.2:3.3.0:4.8.2]
CONTIG3498	36382067_c1_6	4856	18959	1686	562	YJL176C	103	0.05	Saccharomyces cerevisiae	[ui:yj1176c] [pn:transcription regulatory protein:transcription regulatory protein swi3:swi/snf complex component swi3:transcription factor tye2] [gn:swi3:tye2:j0495] [gtcf:10.1:10.2:12.13:12.9] [keggfc:14.2] [sgdfc:1.5.2:3.3.0:4.8.2]
CONTIG4493	24508433_f2_3	4857	18960	2754	918	YJL176C	414	2.1(10)-65	Saccharomyces cerevisiae	[ui:yj1176c] [pn:transcription regulatory protein:transcription regulatory protein swi3:swi/snf complex component swi3:transcription factor tye2] [gn:swi3:tye2:j0495] [gtcf:10.1:10.2:12.13:12.9] [keggfc:14.2] [sgdfc:1.5.2:3.3.0:4.8.2]

CONTIG4854	36025277_f2_1	4858	18961	1413	471	YJL127C	475	6.2(10)-66	Saccharomyces cerevisiae	[ui:yjl127c] [pn:transcription regulatory protein:spt10 protein] [gn:spt10:sud1:crel:j0702] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
b3x13313.y	53836_c3_3	4859	18962	576	192	YJL127C	108	0.00092	Saccharomyces cerevisiae	[ui:yjl127c] [pn:transcription regulatory protein:spt10 protein] [gn:spt10:sud1:crel:j0702] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5539	3913925_f1_1	4860	18963	2226	742	YJL090C	255	1.2(10)-22	Saccharomyces cerevisiae	[ui:yjl090c] [pn:involved in dna replication and s-phase checkpoint:hypothetical 87.2 kd protein in srs2-sip4 intergenic region] [gn:dpb11:j0918] [gtcf:10.1:10.2:10.8:12.8] [keggf:13.2] [sgdfc:3.6.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2690	4882175_f1_1	4861	18964	1317	439	YJL089W	209	6.0(10)-14	Saccharomyces cerevisiae	[ui:yjl089w] [pn:interacts with snf1 protein kinase:sip4 protein] [gn:sip4:j0922] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2958	14650187_c1_2	4862	18965	1491	497	YJL081C	505	1.3(10)-71	Saccharomyces cerevisiae	[ui:yjl081c] [pn:actin-related protein:actin-like protein act3] [gn:arp4:act3:j1012] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5135	36354678_c1_17	4863	18966	510	170	YJL080C	257	9.0(10)-21	Saccharomyces cerevisiae	[ui:yj080c] [pn:histone-like protein:scp160 protein:protein hx] [gn:scp160:hx:j1017] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5135	12922152_c3_20	4864	18967	2499	833	YJL080C	914	8.3(10)-92	Saccharomyces cerevisiae	[ui:yj080c] [pn:histone-like protein:scp160 protein:protein hx] [gn:scp160:hx:j1017] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5522	507186_c1_20	4865	18968	1635	545	YJL061W	132	3.6(10)-5	Saccharomyces cerevisiae	[ui:yj061w] [pn:nuclear pore protein:nucleoporin nup82:nuclear pore protein nup82] [gn:nup82:j1135:hrb187] [gtcf:10.1:10.2:12.3] [keggfc:14.2] [sgdfc:4.11.0.8.1.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG140	515762_c2_2	4866	18969	243	81	YJL050W	187	2.2(10)-13	Saccharomyces cerevisiae	[ui:yj050w] [pn:involved in nucleocytoplasmic transport of mrna:hypothetical helicase in tdh1-gyp6 intergenic region] [gn:mr4:j1158] [gtcf:10.1:10.2:12.3] [keggfc:14.2] [sgdfc:4.11.0.8.1.0.9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4785	33492200_f2_2	4867	18970	516	172	YJL050W	494	3.2(10)-46	Saccharomyces cerevisiae	[ui:yj1050w] [pn:involved in nucleocytoplasmic transport of mma:hypothetical helicase in tdl1-gyp6 intergenic region] [gn:mitr4:j1158] [gtcf:10.1:10.2:12.3] [keggf:14.2] [sgdfc:4.1:0.8:1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5293	26351677_f2_2	4868	18971	2757	919	YJL050W	2832	4.7(10)-295	Saccharomyces cerevisiae	[ui:yj1050w] [pn:involved in nucleocytoplasmic transport of mma:hypothetical helicase in tdl1-gyp6 intergenic region] [gn:mitr4:j1158] [gtcf:10.1:10.2:12.3] [keggf:14.2] [sgdfc:4.1:0.8:1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3153	32553328_f3_1	4869	18972	366	122	YJL041W	109	3.3(10)-5	Saccharomyces cerevisiae	[ui:yj1041w] [pn:nuclear pore protein:nucleoporin nsp1:nuclear pore protein:nsp1:nucleoskeletal-like protein:p110] [gn:nsp1:j1207] [gtcf:10.1] [keggf:14.2] [sgdfc:4.7:0.8:1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5819	22522577_f2_7	4870	18973	1314	438	YJL025W	322	1.0(10)-28	Saccharomyces cerevisiae	[ui:yj1025w] [pn:polymerase i specific transcription initiation factor:ma polymerase i specific transcription initiation factor rrm7] [gn:rm7:j1273] [gtcf:10.1:10.2:10.3] [keggf:14.2] [sgdfc:4.1:0.9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4926	23554843_f2_3	4871	18974	1041	347	YJR035W	1128	1.8(10)-114	Saccharomyces cerevisiae	[ui:yjr035w] [pn:dna repair and recombination protein: dna repair and recombination protein rad26] [gn:rad26: gta1085:j1606] [gicfc:10.1:10.2:10.8] [keggfc:14.2] [sgdgc:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4926	1212937_f3_5	4872	18975	1575	525	YJR035W	921	1.5(10)-92	Saccharomyces cerevisiae	[ui:yjr035w] [pn:dna repair and recombination protein: dna repair and recombination protein rad26] [gn:rad26: gta1085:j1606] [gicfc:10.1:10.2:10.8] [keggfc:14.2] [sgdgc:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3117	14542311_c3_9	4873	18976	1101	367	YJR042W	154	6.4(10)-8	Saccharomyces cerevisiae	[ui:yjr042w] [pn:nuclear pore protein: nucleoporin nup85: nuclear pore protein nup85] [gn:nup85: rat9:j1624] [gicfc:10.1:10.2:10.6] [keggfc:14.2] [sgdgc:4.5.0:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4183	14640660_f1_1	4874	18977	1191	397	YJR042W	283	8.5(10)-23	Saccharomyces cerevisiae	[ui:yjr042w] [pn:nuclear pore protein: nucleoporin nup85: nuclear pore protein nup85] [gn:nup85: rat9:j1624] [gicfc:10.1:10.2:10.6] [keggfc:14.2] [sgdgc:4.5.0:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5049	23834438_c1_13	4875	18978	366	122	YJR052W	192	2.5(10)-14	Saccharomyces cerevisiae	[ui:yjr052w] [pn:nucleotide excision repair protein:dna repair protein rad7] [gn:rad7:j1665] [gtcf:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5049	33337805_c1_12	4876	18979	1596	532	YJR052W	524	2.7(10)-55	Saccharomyces cerevisiae	[ui:yjr052w] [pn:nucleotide excision repair protein:dna repair protein rad7] [gn:rad7:j1665] [gtcf:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5280	32220142_f2_5	4877	18980	747	249	YJR060W	324	2.7(10)-29	Saccharomyces cerevisiae	[ui:yjr060w] [pn:kinetochore protein:centromere-binding protein 1:cbp-1:centromere-binding factor 1] [gn:cbf1:cpf1:cep1:j1730] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:1.1.2:3.8.0:4.8.2:9.5.0:9.6.0]
CONTIG1577	2066431_c2_5	4878	18981	186	62	YJR068W	126	1.3(10)-7	Saccharomyces cerevisiae	[ui:yjr068w] [pn:dna replication factor c, 41 kd subunit:activator 1 41 kd subunit:replication factor c 41 kd subunit] [gn:rfc2:j1808] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3110	12597803_c3_8	4879	18982	741	247	YJR068W	622	7.2(10)-61	Saccharomyces cerevisiae	[ui:yjr068w] [pn:dna replication factor c, 41 kd subunit:activator 1 kd subunit:replication factor c 41 kd subunit] [gn:rfc2:j1808] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3182	448958_c2_8	4880	18983	693	231	YJR093C	202	3.7(10)-16	Saccharomyces cerevisiae	[ui:yjr093c] [pn:component of pre-mrna polyadenylation factor pf i:flp1 protein] [gn:flp1:j1911] [gtcf:10.1:10.2:10.9] [keggfc:14.2] [sgdfc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5518	36503155_fl_1	4881	18984	654	218	YJR112W	177	1.0(10)-13	Saccharomyces cerevisiae	[ui:yjr112w] [pn:nuclear envelope protein:hypothetical 23.6 kd protein in cpa2-atp2 intergenic region] [gn:nfl1:j2011] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5351	19562875_c3_13	4882	18985	1023	341	YJR122W	280	4.5(10)-24	Saccharomyces cerevisiae	[ui:yjr122w] [pn:ccr4 associated factor:hypothetical 57.1 kd protein in atp2-rps5 intergenic region] [gn:caf17:j2043] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1075	24666043_f2_1	4883	18986	870	290	YKL210W	924	7.2(10)-93	Saccharomyces cerevisiae	[ui:ykl210w] [pn:ubiquitin--protein ligase:ubiquitin-activating enzyme e1 1] [gn:uba1] [gtcf:10.1:10.1:10.2:10.7:13.2] [keggfc:14.2] [sgdfc:6.3.0:6.5.1:9.2.0:9.5.0:11.1.0] [db:gtc-saccharomyces cerevisiae]

b1x13259.x	11024166_f2_2	4884	18987	216	72	YKL210W	122	1.8(10)-6	Saccharomyces cerevisiae	[ui:ykl210w] [pn:ubiquitin--protein ligase:ubiquitin-activating enzyme e1 1] [gn:ubal] [gtcf:10.1:10.11:10.2:10.7:13.2] [keggfc:14.2] [sgdfc:6.3.0:6.5.1:9.2.0:9.5.0:11.1.0] [db:gtc-saccharomyces cerevisiae]
b1x13259.x	3923451_f3_3	4885	18988	747	249	YKL210W	808	1.3(10)-80	Saccharomyces cerevisiae	[ui:ykl210w] [pn:ubiquitin--protein ligase:ubiquitin-activating enzyme e1 1] [gn:ubal] [gtcf:10.1:10.11:10.2:10.7:13.2] [keggfc:14.2] [sgdfc:6.3.0:6.5.1:9.2.0:9.5.0:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5818	34491277_c1_32	4886	18989	1080	360	YKL205W	214	1.2(10)-14	Saccharomyces cerevisiae	[ui:ykl205w] [pn:pre-tma splicing protein:protein] [gn:tos1] [gtcf:10.1:10.2:10.6:12.3] [keggfc:14.2] [sgdfc:4.5.0:4.11.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5818	272813_c2_41	4887	18990	1773	591	YKL205W	488	1.5(10)-45	Saccharomyces cerevisiae	[ui:ykl205w] [pn:pre-tma splicing protein:protein] [gn:tos1] [gtcf:10.1:10.2:10.6:12.3] [keggfc:14.2] [sgdfc:4.5.0:4.11.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2637	33725012_f3_1	4888	18991	1083	361	YKL193C	91	0.16	Saccharomyces cerevisiae	[ui:ykl193c] [pn:regulatory subunit for the mitotic function of type i protein phosphatase:protein phosphatases ppl regulatory subunit sds22] [gn:sds22:egp1] [gtcf:10.1:10.2:10.7:12.8] [keggfc:13.3] [sgdfc:3.8.0:6.3.0:9.5.0] [db:gtc-
CONTIG4464	470306_f2_2	4889	18992	1512	504	YKL193C	149	1.2(10)-7	Saccharomyces cerevisiae	[ui:ykl193c] [pn:regulatory subunit for the mitotic function of type i protein phosphatase:protein phosphatases ppl regulatory subunit sds22] [gn:sds22:egp1] [gtcf:10.1:10.2:10.7:12.8] [keggfc:13.3] [sgdfc:3.8.0:6.3.0:9.5.0] [db:gtc-
CONTIG4718	32206956_f2_1	4890	18993	2154	718	YKL193C	139	2.2(10)-6	Saccharomyces cerevisiae	[ui:ykl193c] [pn:regulatory subunit for the mitotic function of type i protein phosphatase:protein phosphatases ppl regulatory subunit sds22] [gn:sds22:egp1] [gtcf:10.1:10.2:10.7:12.8] [keggfc:13.3] [sgdfc:3.8.0:6.3.0:9.5.0] [db:gtc-

CONTIG5101	26375392_fl_1	4891	18994	1431	477	YKL193C	100	0.014	Saccharomyces cerevisiae	[ui:ykl193c] [pn:regulatory subunit for the mitotic function of type i protein phosphatase:protein phosphatases ppl regulatory subunit sds22] [gn:sds22:egp1] [gtcf:10.1:10.2:10.7:12.8] [keggfc:13.3] [sgdfc:3.8.0:6.3.0:9.5.0] [db:gtc-
CONTIG5479	20157632_f2_6	4892	18995	657	219	YKL193C	94	0.032	Saccharomyces cerevisiae	[ui:ykl193c] [pn:regulatory subunit for the mitotic function of type i protein phosphatase:protein phosphatases ppl regulatory subunit sds22] [gn:sds22:egp1] [gtcf:10.1:10.2:10.7:12.8] [keggfc:13.3] [sgdfc:3.8.0:6.3.0:9.5.0] [db:gtc-
CONTIG5506	25523502_c3_15	4893	18996	918	306	YKL193C	342	5.5(10)-55	Saccharomyces cerevisiae	[ui:ykl193c] [pn:regulatory subunit for the mitotic function of type i protein phosphatase:protein phosphatases ppl regulatory subunit sds22] [gn:sds22:egp1] [gtcf:10.1:10.2:10.7:12.8] [keggfc:13.3] [sgdfc:3.8.0:6.3.0:9.5.0] [db:gtc-

CONTIG5644	4394002_fl_2	4894	18997	2145	715	YKL193C	90	0.46	Saccharomyces cerevisiae	[ui:ykl193c] [pn:regulatory subunit for the mitotic function of type i protein phosphatase:protein phosphatases ppl regulatory subunit sds22] [gn:sds22:egp1] [gtcf:10.1:10.2:10.7:12.8] [keggfc:13.3] [sgdfe:3.8.0.6.3.0:9.5.0] [db:gtc-
CONTIG5815	16438261_c3_48	4895	18998	540	180	YKL186C	222	1.8(10)-18	Saccharomyces cerevisiae	[ui:ykl186c] [pn:mna transport protein:mna transport regulator] [gn:mtr2] [gtcf::12.3:10.1:10.2] [keggfc:14.2] [sgdfe:4.11.0.8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5667	5945317_fl_2	4896	18999	1083	361	YKL114C	1098	2.6(10)-111	Saccharomyces cerevisiae	[ui:ykl114c] [pn:dna:apurinic or apyrimidinic site lyase:ap endonuclease:apurinic-apyrimidinic endonuclease] [gn:apn1:ykl513] [gtcf:10.1:10.10:10.2:14.1] [ec:4.2.99.18] [keggfc:14.1] [sgdfe:9.5.0:11.2.1] [db:gtc-saccharomyces cerevi
CONTIG2060	16204092_fl_1	4897	19000	1104	368	YKL109W	95	0.12	Saccharomyces cerevisiae	[ui:ykl109w] [pn:ccat-binding factor subunit:hap4 transcriptional activator] [gn:hap4:ykl465] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfe:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3756	11756387_c2_7	4898	19001	1575	525	YKL109W	95	0.19	Saccharomyces cerevisiae	[ui:ykl109w] [pn:ccaat-binding factor subunit:hap4 transcriptional activator] [gn:hap4:ykl465] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5791	165882_fl_1	4899	19002	1566	522	YKL089W	207	4.9(10)-21	Saccharomyces cerevisiae	[ui:ykl089w] [pn:required for normal chromosome segregation and spindle integrity:protein] [gn:mif2] [gtcf:10.1:10.2:12.8:14.1] [ec:3.4.24.64] [keggf:14.1] [sgdfc:3.8.0:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5100	14073342_c3_8	4900	19003	309	103	YKL074C	125	3.6(10)-7	Saccharomyces cerevisiae	[ui:ykl074c] [pn:pre-mrna splicing factor:splicing factor mud2] [gn:mud2:ykl358] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5189	13103542_fl_1	4901	19004	387	129	YKL062W	153	4.5(10)-10	Saccharomyces cerevisiae	[ui:ykl062w] [pn:transcriptional activator:zinc finger protein:multicopy suppressor of snf1 protein 4] [gn:msn4] [gtcf:10.1:10.2:12.13:13.2] [keggf:14.2] [sgdfc:1.5.2:4.8.2:9.5.0:11.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5755	10970308_f3_10	4902	19005	2283	761	YKL062W	181	9.0(10)-11	Saccharomyces cerevisiae	[ui:ykl062w] [pn:transcriptional activator:zinc finger protein:multicopy suppressor of snf1 protein 4] [gn:msn4] [gtcf:10.1:10.2:12.13:13.2] [keggfc:14.2] [sgdfc:1.5.2:4.8.2:9.5.0:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4060	11878775_f3_3	4903	19006	492	164	YKL058W	318	1.2(10)-28	Saccharomyces cerevisiae	[ui:ykl058w] [pn:tfiia subunit:transcription initiation factor, 13.5 kd:transcription initiation factor iia small chain:tfiia 13.5 kd subunit] [gn:toa2] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3752	21507692_c2_4	4904	19007	2121	707	YKL038W	167	6.5(10)-9	Saccharomyces cerevisiae	[ui:ykl038w] [pn:regulator of glucose-induced genes:putative 128.2 kd transcriptional regulatory protein in ptm1-ixr1 intergenic region] [gn:rgt1:ykl251] [gtcf:10.1:10.2:12.13] [keggfc:14.2] [sgdfc:1.5.2:4.8.2:9.5.0] [db:gtc-saccharo]
CONTIG4152	26443927_c1_6	4905	19008	1230	410	YKL028W	639	1.2(10)-62	Saccharomyces cerevisiae	[ui:ykl028w] [pn:tfiie subunit:transcription initiation factor, 66 kd:transcription initiation factor iie, alpha subunit:tfiie-alpha:transcription factor a large subunit:factor a 66 kd subunit] [gn:tfai1] [gtcf:10.1:10.2] [keggfc:14.2]

CONTIG3951	14553275_c1_5	4906	19009	1401	467	YKL022C	748	3.2(10)-74	Saccharomyces cerevisiae	[ui:ykl022c] [pn:subunit of anaphase-promoting complex:cyclosome:cell division control protein 16] [gn:cdc16] [gtcf:10.1:10.11:10.2:12.16:12.8] [keggfc:13.3] [sgdfc:3.8.0:6.5.1:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2112	26290902_f3_3	4907	19010	1443	481	YKL020C	244	2.6(10)-37	Saccharomyces cerevisiae	[ui:ykl020c] [pn:dosage-dependent suppressor of ty-induced promotor mutations:protein] [gn:spi23] [gtcf:10.2] [keggfc:14.2] [sgdfc:9.5.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1305	1961462_c3_4	4908	19011	1089	363	YKL015W	802	6.2(10)-80	Saccharomyces cerevisiae	[ui:ykl015w] [pn:positive activator of the proline utilisation pathway:proline utilization trans-activator] [gn:put3] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3445	54187_c3_6	4909	19012	1524	508	YKL015W	95	0.33	Saccharomyces cerevisiae	[ui:ykl015w] [pn:positive activator of the proline utilisation pathway:proline utilization trans-activator] [gn:put3] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3566	29376655_c2_9	4910	19013	627	209	YKL015W	220	5.9(10)-17	Saccharomyces cerevisiae	[ui:ykl015w] [pn:positive activator of the proline utilisation pathway:proline utilization trans-activator] [gn:put3] [gtcf:10.1:10.2] [keggf:14.2] [sgdfe:1.1.2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3982	18760890_c3_8	4911	19014	1914	638	YKL015W	131	7.5(10)-5	Saccharomyces cerevisiae	[ui:ykl015w] [pn:positive activator of the proline utilisation pathway:proline utilization trans-activator] [gn:put3] [gtcf:10.1:10.2] [keggf:14.2] [sgdfe:1.1.2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4660	21884677_c1_8	4912	19015	696	232	YKL015W	125	1.7(10)-10	Saccharomyces cerevisiae	[ui:ykl015w] [pn:positive activator of the proline utilisation pathway:proline utilization trans-activator] [gn:put3] [gtcf:10.1:10.2] [keggf:14.2] [sgdfe:1.1.2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5235	35432156_c2_17	4913	19016	1128	376	YKL015W	94	0.29999	Saccharomyces cerevisiae	[ui:ykl015w] [pn:positive activator of the proline utilisation pathway:proline utilization trans-activator] [gn:put3] [gtcf:10.1:10.2] [keggf:14.2] [sgdfe:1.1.2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5732	4085937_c2_30	4914	19017	2490	830	YKL015W	126	0.0004	Saccharomyces cerevisiae	[ui:ykl015w] [pn:positive activator of the proline utilisation pathway:proline utilization trans-activator] [gn:put3] [gtcf:10.1:10.2] [keggf:14.2] [sgdfe:1.1.2.4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2948	2613901_c1_4	4915	19018	1203	401	YKL005C	107	0.0051	Saccharomyces cerevisiae	[ui:ykl005c] [pn:weak similarity to ykr029c and d.melanogaster transcription elongation factor dms-ii:hypothetical 67.9 kd protein rpl14a-aur1 intergenic region] [gn:ykl150] [gtcf:10.1:10.2] [keggc:14.2] [sgdfc:4.12.0:9.5.0] [db:gtc]
CONTIG4205	976013_c3_7	4916	19019	888	296	YKL005C	94	0.13	Saccharomyces cerevisiae	[ui:ykl005c] [pn:weak similarity to ykr029c and d.melanogaster transcription elongation factor dms-ii:hypothetical 67.9 kd protein rpl14a-aur1 intergenic region] [gn:ykl150] [gtcf:10.1:10.2] [keggc:14.2] [sgdfc:4.12.0:9.5.0] [db:gtc]
CONTIG5102	26441557_c2_5	4917	19020	387	129	YKL005C	172	3.7(10)-12	Saccharomyces cerevisiae	[ui:ykl005c] [pn:weak similarity to ykr029c and d.melanogaster transcription elongation factor dms-ii:hypothetical 67.9 kd protein rpl14a-aur1 intergenic region] [gn:ykl150] [gtcf:10.1:10.2] [keggc:14.2] [sgdfc:4.12.0:9.5.0] [db:gtc]
CONTIG1056	21490677_c2_2	4918	19021	738	246	YKR002W	892	1.8(10)-89	Saccharomyces cerevisiae	[ui:ykr002w] [pn:poly:a polymerase] [gn:pap1] [gtcf:10.1:10.2:10.9:14.1] [ec:2.7.7.19] [keggc:14.1] [sgdfc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2615	393775_f2_1	4919	19022	1353	451	YKR002W	1446	3.5(10)-148	Saccharomyces cerevisiae	[ui:ykr002w] [pn:poly:a polymerase] [gn:pap1] [gtcf:10.1:10.2:10.9:14.1] [ec:2.7.7.19] [keggf:14.1] [sgdfc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG911	24609517_f3_1	4920	19023	453	151	YKR002W	128	1.8(10)-7	Saccharomyces cerevisiae	[ui:ykr002w] [pn:poly:a polymerase] [gn:pap1] [gtcf:10.1:10.2:10.9:14.1] [ec:2.7.7.19] [keggf:14.1] [sgdfc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
b2x15963.y	4792178_f3_1	4921	19024	492	164	YKR008W	149	1.2(10)-9	Saccharomyces cerevisiae	[ui:ykr008w] [pn:similarity to s.pombe and chicken bromodomain proteins:hypothetical 72.3 kd protein in mrp13-fox2 intergenic region] [gn:yk107] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1427	7111541_f1_1	4922	19025	252	84	YKR054C	98	0.00289	Saccharomyces cerevisiae	[ui:ykr054c] [pn:dyn1:heavy chain, cytosolic:dyhc] [gn:dyn1:dhcl] [gtcf:10.1:10.2:12.10:12.16:12.8] [keggf:14.2] [sgdfc:3.8.0:8.3.0:8.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1427	29330380_f1_2	4923	19026	1104	368	YKR054C	648	1.2(10)-61	Saccharomyces cerevisiae	[ui:ykr054c] [pn:dynein heavy chain, cytosolic:dyhc] [gn:dyn1:dhc1] [gtcf:10.1:10.2:12.10:12.16:12.8] [keggfc:14.2] [sgdgc:3.8:0.8:3.0:8.8:0.9:3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1148	6303188_c2_2	4924	19027	612	204	YKR054C	401	2.0(10)-35	Saccharomyces cerevisiae	[ui:ykr054c] [pn:dynein heavy chain, cytosolic:dyhc] [gn:dyn1:dhc1] [gtcf:10.1:10.2:12.10:12.16:12.8] [keggfc:14.2] [sgdgc:3.8:0.8:3.0:8.8:0.9:3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4169	19822202_c2_3	4925	19028	2328	776	YKR054C	1077	3.5(10)-107	Saccharomyces cerevisiae	[ui:ykr054c] [pn:dynein heavy chain, cytosolic:dyhc] [gn:dyn1:dhc1] [gtcf:10.1:10.2:12.10:12.16:12.8] [keggfc:14.2] [sgdgc:3.8:0.8:3.0:8.8:0.9:3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2880	972203_f3_1	4926	19029	1224	408	YKR054C	271	1.2(10)-27	Saccharomyces cerevisiae	[ui:ykr054c] [pn:dynein heavy chain, cytosolic:dyhc] [gn:dyn1:dhc1] [gtcf:10.1:10.2:12.10:12.16:12.8] [keggfc:14.2] [sgdgc:3.8:0.8:3.0:8.8:0.9:3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4797	4801525_c3_4	4927	19030	1467	489	YKR054C	248	4.5(10)-17	Saccharomyces cerevisiae	[ui:ykr054c] [pn:dyn1:dhc] chain, cytosolic:dyhc [gn:dyn1:dhc] [gicf:10.1:10.2:12.10:12.16:12.8] [keggf:14.2] [sgdfc:3.8.0.8.3.0.8.0.9.3.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5802	22476703_c3_36	4928	19031	423	141	YKR054C	169	8.5(10)-11	Saccharomyces cerevisiae	[ui:ykr054c] [pn:dyn1:dhc] chain, cytosolic:dyhc [gn:dyn1:dhc] [gicf:10.1:10.2:12.10:12.16:12.8] [keggf:14.2] [sgdfc:3.8.0.8.3.0.8.0.9.3.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
b9x13862.x	23555426_f3_1	4929	19032	396	132	YKR054C	293	5.9(10)-24	Saccharomyces cerevisiae	[ui:ykr054c] [pn:dyn1:dhc] chain, cytosolic:dyhc [gn:dyn1:dhc] [gicf:10.1:10.2:12.10:12.16:12.8] [keggf:14.2] [sgdfc:3.8.0.8.3.0.8.0.9.3.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5328	7070312_c3_18	4930	19033	1665	555	YKR056W	1260	1.8(10)-128	Saccharomyces cerevisiae	[ui:ykr056w] [pn:endo-exonuclease:endo-exonuclease nuc] [gn:mcl:nud1] [gicf:10.1:10.10:10.2:10.8:14.1] [ec:3.-.-.] [keggf:14.1] [sgdfc:3.7.0.9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG3280	6064135_f3_4	4931	19034	423	141	YKR062W	352	3.0(10)-32	Saccharomyces cerevisiae	[ui:ykr062w] [pn:tfie subunit:transcription initiation factor, 43 kd:transcription initiation factor iic, beta subunit:tfie-beta:transcription factor a small subunit:factor a 43 kd subunit] [gn:ifa2] [gtcf:10.1:10.2] [keggfc:14.2]
CONTIG5588	14157757_c2_13	4932	19035	771	257	YKR063C	381	2.5(10)-35	Saccharomyces cerevisiae	[ui:ykr063c] [pn:involved in cell morphogenesis, cytoskeletal regulation and bud formation:protein] [gn:las1] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.2.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3308	3020818_c3_4	4933	19036	1377	459	YKR072C	292	7.0(10)-24	Saccharomyces cerevisiae	[ui:ykr072c] [pn:involved in cell cycle-specific gene expression:sis2 protein:halotolerance protein hal3] [gn:sis2:hal3] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1054	957875_f3_4	4934	19037	621	207	YKR082W	99	0.041	Saccharomyces cerevisiae	[ui:ykr082w] [pn:nuclear pore protein:nucleoporin nup133:nuclear pore protein nup133] [gn:nup133:ykr402] [gtcf:10.1:10.2:12.3] [keggfc:14.2] [sgdgc:4.1.0:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2223	23673186_c1_4	4935	19038	819	273	YKR082W	102	0.03699	Saccharomyces cerevisiae	[ui:ykr082w] [pn:nuclear pore protein:nucleoporin nup133:nuclear pore protein nup133] [gn:nup133:ykr402] [gtcf:10.1:10.2:12.3] [keggfc:14.2] [sgdfc:4.11.0:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5159	12286705_f2_3	4936	19039	726	242	YKR086W	372	3.7(10)-33	Saccharomyces cerevisiae	[ui:ykr086w] [pn:ma-dependent atpase:pre-mrna splicing factor rna helicase prp16] [gn:prp16:ykr406] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3107	35291466_f2_1	4937	19040	2172	724	YKR086W	1200	1.8(10)-127	Saccharomyces cerevisiae	[ui:ykr086w] [pn:ma-dependent atpase:pre-mrna splicing factor rna helicase prp16] [gn:prp16:ykr406] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4377	34172162_f2_1	4938	19041	2262	754	YKR092C	98	0.00048	Saccharomyces cerevisiae	[ui:ykr092c] [pn:suppressor of mutant ac40 of rna polymerase i and iii:suppressor protein srp40] [gn:srp40:ykr412a] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4393	24018807_c1_7	4939	19042	1248	416	YKR092C	98	0.047.	Saccharomyces cerevisiae	[ui:ykr092c] [pn:suppressor of mutant ac40 of rna polymerase i and iii:suppressor protein srp40] [gn:srp40-ykr412a] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.12.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5299	4867180_f1_2	4940	19043	3681	1227	YKR092C	108	0.01499	Saccharomyces cerevisiae	[ui:ykr092c] [pn:suppressor of mutant ac40 of rna polymerase i and iii:suppressor protein srp40] [gn:srp40-ykr412a] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.12.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5594	43550787_f3_8	4941	19044	2511	837	YKR092C	107	0.012	Saccharomyces cerevisiae	[ui:ykr092c] [pn:suppressor of mutant ac40 of rna polymerase i and iii:suppressor protein srp40] [gn:srp40-ykr412a] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.12.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5660	24020325_c2_22	4942	19045	2130	710	YKR092C	99	0.04299	Saccharomyces cerevisiae	[ui:ykr092c] [pn:suppressor of mutant ac40 of rna polymerase i and iii:suppressor protein srp40] [gn:srp40-ykr412a] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.12.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5706	26772711_c3_25	4943	19046	1245	415	YKR092C	358	6.9(10)-33	Saccharomyces cerevisiae	[ui:ykr092c] [pn:suppressor of mutant ac40 of rna polymerase i and iii:suppressor protein srp40] [gn:srp40-ykr412a] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.12.0:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG759	10945193_f1_1	4944	19047	1185	395	YKR092C	98	0.047	Saccharomyces cerevisiae	[ui:ykr092c] [pn:suppressor of mutant ac40 of rna polymerase i and iii:suppressor protein srp40] [gn:srp40:ykr412a] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1263	979711_f1_4	4945	19048	378	126	YKR095W	99	0.001	Saccharomyces cerevisiae	[ui:ykr095w] [pn:myosin-like protein related to uo1p:myosin-like protein mlp1] [gn:mlp1:ykr415] [gtcf:10.1:10.10:10.2] [keggf:14.2] [sgdf:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1719	23438942_f2_1	4946	19049	855	285	YKR095W	91	0.65	Saccharomyces cerevisiae	[ui:ykr095w] [pn:myosin-like protein related to uo1p:myosin-like protein mlp1] [gn:mlp1:ykr415] [gtcf:10.1:10.10:10.2] [keggf:14.2] [sgdf:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2276	24431336_f3_2	4947	19050	1062	354	YKR095W	106	0.028	Saccharomyces cerevisiae	[ui:ykr095w] [pn:myosin-like protein related to uo1p:myosin-like protein mlp1] [gn:mlp1:ykr415] [gtcf:10.1:10.10:10.2] [keggf:14.2] [sgdf:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2699	24492005_f1_1	4948	19051	738	246	YKR095W	123	0.00012	Saccharomyces cerevisiae	[ui:ykr095w] [pn:myosin-like protein related to uo1p:myosin-like protein mlp1] [gn:mlp1:ykr415] [gtcf:10.1:10.10:10.2] [keggf:14.2] [sgdf:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG3289	19573957_f1_1	4949	19052	1110	370	YKR095W	133	4.5(10)-5	Saccharomyces cerevisiae	[ui:ykr095w] [pn:myosin-like protein related to uso1p:myosin-like protein mlp1] [gn:mlp1:ykr415] [gicfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5.0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG3870	9861078_f3_1	4950	19053	2229	743	YKR095W	176	1.5(10)-12	Saccharomyces cerevisiae	[ui:ykr095w] [pn:myosin-like protein related to uso1p:myosin-like protein mlp1] [gn:mlp1:ykr415] [gicfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5.0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG4435	1379415_f2_5	4951	19054	792	264	YKR095W	123	0.00019	Saccharomyces cerevisiae	[ui:ykr095w] [pn:myosin-like protein related to uso1p:myosin-like protein mlp1] [gn:mlp1:ykr415] [gicfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5.0:11.2.1] [db:gic-saccharomyces cerevisiae]
CONTIG5711	34187660_f3_7	4952	19055	2574	858	YKR095W	93	0.68	Saccharomyces cerevisiae	[ui:ykr095w] [pn:myosin-like protein related to uso1p:myosin-like protein mlp1] [gn:mlp1:ykr415] [gicfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5.0:11.2.1] [db:gic-saccharomyces cerevisiae]
b9x10449.y	26773516_c3_2	4953	19056	516	172	YKR095W	163	1.6(10)-10	Saccharomyces cerevisiae	[ui:ykr095w] [pn:myosin-like protein related to uso1p:myosin-like protein mlp1] [gn:mlp1:ykr415] [gicfc:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5.0:11.2.1] [db:gic-saccharomyces cerevisiae]

b9x11865.x	1050933_c1_2	4954	19057	819	273	YKR095W	182	1.5(10)-12	Saccharomyces cerevisiae	[ui:ykr095w] [pn:myosin-like protein mlp1] [gn:mlp1:ykr415] [gtcf:10.1:10.10:10.2] [keggc:14.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5679	25594034_c2_19	4955	19058	690	230	YKR095W	93	0.29999	Saccharomyces cerevisiae	[ui:ykr095w] [pn:myosin-like protein mlp1] [gn:mlp1:ykr415] [gtcf:10.1:10.10:10.2] [keggc:14.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
b2x10471.y	9807969_c2_2	4956	19059	789	263	YKR095W	103	0.033	Saccharomyces cerevisiae	[ui:ykr095w] [pn:myosin-like protein mlp1] [gn:mlp1:ykr415] [gtcf:10.1:10.10:10.2] [keggc:14.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5544	4098427_c1_16	4957	19060	951	317	YKR099W	551	4.7(10)-53	Saccharomyces cerevisiae	[ui:ykr099w] [pn:transcription factor:myb-like dna-binding protein] [gn:bas1] [gtcf:10.1:10.2] [keggc:14.2] [sgdfc:1.1.2:1.3.5:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4661	10626412_f2_2	4958	19061	273	91	YLL039C	164	1.2(10)-11	Saccharomyces cerevisiae	[ui:yll039c] [pn:ubiquitin precursor] [gn:ubi4] [gtcf:10.1:10.11:10.2:10.7:12.15:12.16:13.2] [keggc:14.2] [sgdfc:3.4.0:5.5.0:6.4.0:6.5.1:9.2.0:9.5.0:11.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5683	13834636_c2_22	4959	19062	714	238	YLL039C	1141	7.2(10)-116	Saccharomyces cerevisiae	[ui:yll039c] [pn:ubiquitin precursor] [gn:ubi4] [gicf:10.1:10.1:10.2:10.7:12.15:12.16:13.2] [keggf:14.2] [sgdgc:3.4.0:5.0:6.4.0:6.5.1:9.2.0:9.5.0:11.1.0] [db:gic-saccharomyces cerevisiae]
CONTIG4777	3907830_c3_10	4960	19063	891	297	YLL036C	252	5.7(10)-21	Saccharomyces cerevisiae	[ui:yll036c] [pn:non-nrnp sliceosome component required for dna repair:pre-rna splicing factor prp19] [gn:prp19:ps04] [gicf:10.1:10.2] [keggf:14.2] [sgdgc:4.9.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG1469	26692142_f3_2	4961	19064	444	148	YLL011W	95	0.01	Saccharomyces cerevisiae	[ui:yll011w] [pn:involved in 18s pre-rna production:sof1 protein] [gn:sof1:11339] [gicf:10.1:10.2:10.3] [keggf:14.2] [sgdgc:4.2.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5367	23865811_c1_11	4962	19065	741	247	YLL011W	637	1.8(10)-62	Saccharomyces cerevisiae	[ui:yll011w] [pn:involved in 18s pre-rna production:sof1 protein] [gn:sof1:11339] [gicf:10.1:10.2:10.3] [keggf:14.2] [sgdgc:4.2.0:9.5.0] [db:gic-saccharomyces cerevisiae]
CONTIG5792	5079717_f2_6	4963	19066	1719	573	YLL008W	1466	5.7(10)-156	Saccharomyces cerevisiae	[ui:yll008w] [pn:ma helicase of the dead box family:putative atp-dependent ma helicase drs1] [gn:drs1:11345] [gicf:10.1:10.2:10.3:12.16] [keggf:14.2] [sgdgc:4.2.0:6.4.0:9.5.0] [db:gic-saccharomyces cerevisiae]

CONTIG5612	10553426_f2_4	4964	19067	1758	586	YLL004W	120	0.00056	Saccharomyces cerevisiae	[ui:yil004w] [pn:origin recognition complex, 62 kda subunit:origin recognition complex protein, subunit 3:origin recognition complex protein 62 kd subunit] [gn:orc3:oafl:oi1:11365] [gtcf:10.1:10.2:10.8:12.8:12.9] [keggfc:13.2] [sgdf]
CONTIG5612	672342_f3_6	4965	19068	330	110	YLL004W	149	1.2(10)-9	Saccharomyces cerevisiae	[ui:yil004w] [pn:origin recognition complex, 62 kda subunit:origin recognition complex protein, subunit 3:origin recognition complex protein 62 kd subunit] [gn:orc3:oafl:oi1:11365] [gtcf:10.1:10.2:10.8:12.8:12.9] [keggfc:13.2] [sgdf]
CONTIG4626	19938160_cl_4	4966	19069	2445	815	YLR014C	449	6.9(10)-87	Saccharomyces cerevisiae	[ui:yilr014c] [pn:transcription factor regulating pyrimidine pathway:pyrimidine pathway regulatory protein 1] [gn:ppr1] [gtcf:10.1:10.2] [keggfc:14.2] [sgdf:1.3.5:4.8:2.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3082	6027043_fl_1	4967	19070	483	161	YLR025W	135	5.0(10)-9	Saccharomyces cerevisiae	[ui:yilr025w] [pn:nuclear protein] [gn:snf7] [gtcf:10.1:10.2:12.13:12.15] [keggfc:14.2] [sgdf:1.5.2:3.4.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4349	4491052_c3_5	4968	19071	690	230	YLR025W	204	1.3(10)-16	Saccharomyces cerevisiae	[ui:yilr025w] [pn:nuclear protein] [gn:snf7] [gtcf:10.1:10.2:12.13:12.15] [keggfc:14.2] [sgdf:1.5.2:3.4.0.9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5645	24488443_c3_22	4969	19072	3270	1090	YLR032W	1383	8.6(10)-162	Saccharomyces cerevisiae	[ui:ylr032w] [pn:dna helicase:dna repair protein rad5] [gn:rad5:rev2:snm2] [gtcf:10.1:10.10.2:10.8] [keggf:14.2] [sgdf:3.7.0:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5212	33406553_c3_19	4970	19073	1671	557	YLR055C	279	7.0(10)-22	Saccharomyces cerevisiae	[ui:ylr055c] [pn:transcription factor:transcription factor spt8] [gn:spt8:l2144] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5484	12304525_c3_20	4971	19074	4026	1342	YLR086W	1879	4.5(10)-194	Saccharomyces cerevisiae	[ui:ylr086w] [pn:similarity to chromosome condensation proteins] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4418	16412511_f2_6	4972	19075	885	295	YLR098C	115	0.00069	Saccharomyces cerevisiae	[ui:ylr098c] [pn:transcription factor:cha4 activatory protein] [gn:cha4:l8004] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG431	12696886_c3_3	4973	19076	672	224	YLR105C	182	1.2(10)-13	Saccharomyces cerevisiae	[ui:ylr105c] [pn:tma splicing endonuclease beta subunit:tma-splicing endonuclease beta-subunit] [gn:sen2:l8004] [gtcf:10.1:10.2:10.6] [keggf:14.2] [sgdf:4.5.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1820	22850662_c3_3	4974	19077	534	178	YLR131C	227	7.2(10)-18	Saccharomyces cerevisiae	[ui:ylr131c] [pn:metallothionein expression activator] [gn:ace2:13:123:19606] [gtcf:10.1:10.2:12.13:12.8] [keggfc:14.2] [sgdfc:1.5:2.3:9.0:4.8:2.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4941	10979555_c2_6	4975	19078	327	109	YLR147C	280	1.3(10)-24	Saccharomyces cerevisiae	[ui:ylr147c] [pn:strong similarity to small nuclear ribonucleoprotein d3:small nuclear ribonucleoprotein d3 homolog] [gn:smd3:19634] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1039	6646892_c3_5	4976	19079	576	192	YLR175W	638	1.5(10)-62	Saccharomyces cerevisiae	[ui:ylr175w] [pn:centromere/microtubule binding protein:centromere/microtubule binding protein cbf5:p64"] [gn:cbf5:19470] [gtcf:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.1:0:3.8.0:9.3:0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2834	10634652_c3_6	4977	19080	303	101	YLR175W	398	4.0(10)-37	Saccharomyces cerevisiae	[ui:ylr175w] [pn:centromere/microtubule binding protein:centromere/microtubule binding protein cbf5:p64"] [gn:cbf5:19470] [gtcf:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.1:0:3.8.0:9.3:0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1246	13791410_f3_1	4978	19081	1074	358	YLR176C	135	7.4(10)-6	Saccharomyces cerevisiae	[ui:ylr176c] [pn:dna binding protein] [gn:rxf1] [gtcf:10.1:10.2:12.8] [keggfc:13.1] [sgdfe:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4976	6270908_f2_3	4979	19082	2577	859	YLR176C	300	6.5(10)-37	Saccharomyces cerevisiae	[ui:ylr176c] [pn:dna binding protein] [gn:rxf1] [gtcf:10.1:10.2:12.8] [keggfc:13.1] [sgdfe:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1268	15049000_f3_2	4980	19083	993	331	YLR212C	524	2.3(10)-60	Saccharomyces cerevisiae	[ui:ylr212c] [pn:gamma tubulin:tubulin gamma chain] [gn:tub4:18167] [gtcf:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfe:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4646	25423593_f3_2	4981	19084	408	136	YLR212C	105	4.4(10)-5	Saccharomyces cerevisiae	[ui:ylr212c] [pn:gamma tubulin:tubulin gamma chain] [gn:tub4:18167] [gtcf:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfe:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3156	33395062_f3_2	4982	19085	1497	499	YLR234W	819	1.5(10)-112	Saccharomyces cerevisiae	[ui:ylr234w] [pn:dna topoisomerase iii] [gn:top3:edr1:18083] [gtcf:10.1:10.2:12.8:14.1] [ec:5.99.1.2] [keggfc:14.1] [sgdfe:3.5.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4303	2948838_c2_5	4983	19086	1527	509	YLR256W	134	1.8(10)-5	Saccharomyces cerevisiae	[ui:ylr256w] [pn:transcription factor:cyp1 activatory protein] [gn:cyp1:hap1] [gtcf:10.1:10.2] [keggc:14.2] [sgdgc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4762	2757655_f2_6	4984	19087	897	299	YLR256W	105	0.025	Saccharomyces cerevisiae	[ui:ylr256w] [pn:transcription factor:cyp1 activatory protein] [gn:cyp1:hap1] [gtcf:10.1:10.2] [keggc:14.2] [sgdgc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5745	2504676_f2_5	4985	19088	2961	987	YLR256W	120	0.0032	Saccharomyces cerevisiae	[ui:ylr256w] [pn:transcription factor:cyp1 activatory protein] [gn:cyp1:hap1] [gtcf:10.1:10.2] [keggc:14.2] [sgdgc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
b2x10621.y	5163942_f3_2	4986	19089	762	254	YLR256W	165	7.5(10)-11	Saccharomyces cerevisiae	[ui:ylr256w] [pn:transcription factor:cyp1 activatory protein] [gn:cyp1:hap1] [gtcf:10.1:10.2] [keggc:14.2] [sgdgc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2166	4948336_f3_4	4987	19090	747	249	YLR274W	802	6.2(10)-80	Saccharomyces cerevisiae	[ui:ylr274w] [pn:cell division control protein:cell division control protein 46:minichromosome maintenance protein 5] [gn:cdc46:mcm5:i9328] [gtcf:10.1:10.2:10.8:12.8] [keggc:13.2] [sgdgc:3.6.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3544	4351426_f3_5	4988	19091	1290	430	YLR274W	481	1.6(10)-80	Saccharomyces cerevisiae	[ui:ylr274w] [pn:cell division control protein:cell division control maintenance protein 5] [gn:cdc46:mcm5:19328] [gtcf:10.1:10.2:10.8:12.8] [keggf:13.2] [sgdfc:3.6:0.3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2166	22303177_c1_5	4989	19092	444	148	YLR275W	275	4.2(10)-24	Saccharomyces cerevisiae	[ui:ylr275w] [pn:strong similarity to human snmp chain d2 involved in systemic lupus erythematosus] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.9:0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1262	565757_f2_3	4990	19093	939	313	YLR277C	711	2.7(10)-70	Saccharomyces cerevisiae	[ui:ylr277c] [pn:component of pre-mrna polyadenylation factor pf i] [gn:brr5] [gtcf:10.1:10.2:10.9] [keggf:14.2] [sgdfc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
b9x12m23.x	35328538_f3_1	4991	19094	258	86	YLR277C	198	9.5(10)-15	Saccharomyces cerevisiae	[ui:ylr277c] [pn:component of pre-mrna polyadenylation factor pf i] [gn:brr5] [gtcf:10.1:10.2:10.9] [keggf:14.2] [sgdfc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
b9x12m23.x	17007937_f3_2	4992	19095	297	99	YLR277C	95	0.001	Saccharomyces cerevisiae	[ui:ylr277c] [pn:component of pre-mrna polyadenylation factor pf i] [gn:brr5] [gtcf:10.1:10.2:10.9] [keggf:14.2] [sgdfc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG731	390750_f2_1	4993	19096	708	236	YLR293C	1052	2.0(10)-106	Saccharomyces cerevisiae	[ui:ylr293c] [pn:gtp-binding protein of the ras superfamily:gtp-binding nuclear protein gsp1/cnr1] [gn:gsp1:cnr1:cst17:18003] [gtcf:10.1:10.2:12.3] [keggfc:14.2] [sgdfc:4.1:0.8:1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3079	26189181_f1_1	4994	19097	468	156	YLR298C	174	2.2(10)-13	Saccharomyces cerevisiae	[ui:ylr298c] [pn:part of the u1 complex] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3116	6767786_f2_2	4995	19098	1314	438	YLR335W	142	1.8(10)-16	Saccharomyces cerevisiae	[ui:ylr335w] [pn:nucleoporin:nuclear pore protein:p95] [gn:nup2] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:8.1:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4375	24398461_c3_9	4996	19099	1998	666	YLR335W	155	1.3(10)-7	Saccharomyces cerevisiae	[ui:ylr335w] [pn:nucleoporin:nuclear pore protein:p95] [gn:nup2] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:8.1:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5399	26429087_f2_2	4997	19100	762	254	YLR335W	221	2.8(10)-17	Saccharomyces cerevisiae	[ui:ylr335w] [pn:nucleoporin:nuclear pore protein:p95] [gn:nup2] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:8.1:0.9:5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4994	471041_f3_5	4998	19101	1044	348	YLR398C	832	1.8(10)-82	Saccharomyces cerevisiae	[ui:ylr398c] [pn:antiviral protein and putative helicase:antiviral protein] [gn:ski2] [gtcf:10.1:10.2:12.12] [keggf:14.2] [sgdfc:9.5.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5760	4728438_c1_29	4999	19102	2208	736	YLR398C	1757	8.6(10)-199	Saccharomyces cerevisiae	[ui:ylr398c] [pn:antiviral protein and putative helicase:antiviral protein] [gn:ski2] [gtcf:10.1:10.2:12.12] [keggf:14.2] [sgdfc:9.5.0:11.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5733	1210287_f1_1	5000	19103	498	166	YLR403W	128	2.5(10)-7	Saccharomyces cerevisiae	[ui:ylr403w] [pn:zinc finger protein:zinc finger protein sfp1] [gn:sfp1:18084] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.1.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5733	19738337_f2_5	5001	19104	864	288	YLR403W	479	1.8(10)-58	Saccharomyces cerevisiae	[ui:ylr403w] [pn:zinc finger protein:zinc finger protein sfp1] [gn:sfp1:18084] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.1.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3247	866708_f3_3	5002	19105	819	273	YLR430W	193	1.3(10)-12	Saccharomyces cerevisiae	[ui:ylr430w] [pn:positive effector of trna-splicing endonuclease:trna-splicing endonuclease positive effector] [gn:sen1] [gtcf:10.1:10.2:10.6] [keggf:14.2] [sgdfc:4.5.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3653	12985630_c3_8	5003	19106	2400	800	YLR430W	493	5.0(10)-61	Saccharomyces cerevisiae	[ui:ylr430w] [pn:positive effector of trna-splicing endonuclease:trna-splicing endonuclease positive effector] [gn:sen1] [gdcf:10.1:10.2:10.6] [keggf:14.2] [sgdcf:4.5.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4822	975727_f2_6	5004	19107	1218	406	YLR430W	594	2.8(10)-56	Saccharomyces cerevisiae	[ui:ylr430w] [pn:positive effector of trna-splicing endonuclease:trna-splicing endonuclease positive effector] [gn:sen1] [gdcf:10.1:10.2:10.6] [keggf:14.2] [sgdcf:4.5.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
b1x10463.y	32244792_f2_1	5005	19108	729	243	YLR430W	392	8.8(10)-35	Saccharomyces cerevisiae	[ui:ylr430w] [pn:positive effector of trna-splicing endonuclease:trna-splicing endonuclease positive effector] [gn:sen1] [gdcf:10.1:10.2:10.6] [keggf:14.2] [sgdcf:4.5.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5665	2915831_f2_3	5006	19109	2970	990	YLR451W	919	4.0(10)-121	Saccharomyces cerevisiae	[ui:ylr451w] [pn:transcription factor:regulatory protein leu3] [gn:leu3:19324] [gdcf:10.1:10.2] [keggf:14.2] [sgdcf:1.1.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5199	4475886_c1_9	5007	19110	3396	1132	YML103C	522	1.6(10)-61	Saccharomyces cerevisiae	[ui:yml103c] [pn:nucleoporin:nuclear pore protein] [gn:nup188] [gdcf:10.1:10.2] [keggf:14.2] [sgdcf:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

b9x11910.y	31304582_f3_1	5008	19111	816	272	YML103C	354	6.5(10)-31	Saccharomyces cerevisiae	[ui:ym1103c] [pn:nucleoporin:nuclear pore protein] [gn:nup188] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:8.1:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3719	24804033_f3_4	5009	19112	249	83	YML103C	93	0.0038	Saccharomyces cerevisiae	[ui:ym1103c] [pn:nucleoporin:nuclear pore protein] [gn:nup188] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:8.1:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5722	6287811_f2_6	5010	19113	537	179	YML098W	166	1.5(10)-12	Saccharomyces cerevisiae	[ui:ym1098w] [pn:tfiid subunit:ibp-associated factor, 19 kd:protein] [gn:taf19:fun81] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4302	20422716_c1_4	5011	19114	2253	751	YML076C	277	1.3(10)-40	Saccharomyces cerevisiae	[ui:ym1076c] [pn:weak similarity to transcription factor] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3857	803758_f3_4	5012	19115	315	105	YML074C	130	7.0(10)-8	Saccharomyces cerevisiae	[ui:ym1074c] [pn:proline cis-trans isomerase:fk506-binding nuclear protein:peptidyl-prolyl cis- trans isomerase:ppiase:proline rotamase:nucleolar proline isomerase:fkbp-70] [gn:fpr3:npi46] [gtcf:10.1:10.2:10.5:10.7:12.7:14.1] [ec:5.2]

CONTIG4014	9776061_f3_5	5013	19116	699	233	YML069W	591	1.3(10)-57	Saccharomyces cerevisiae	[ui:ym1069w] [pn:similarity to hmg proteins] [gn:pob3] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:9.5:0.9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4014	25948302_f3_6	5014	19117	207	69	YML069W	146	2.1(10)-9	Saccharomyces cerevisiae	[ui:ym1069w] [pn:similarity to hmg proteins] [gn:pob3] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:9.5:0.9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1481	23836502_c3_8	5015	19118	753	251	YML065W	201	5.7(10)-15	Saccharomyces cerevisiae	[ui:ym1065w] [pn:origin recognition complex, 104 kd subunit:origin recognition complex protein, subunit 1:origin recognition complex protein 120 kd subunit] [gn:orc1] [gtcf:10.1:10.2:10.8:12.8:12.9] [keggf:13.2] [sgdfc:3.3.0.3.6.0.4]
CONTIG4399	14746043_f2_2	5016	19119	990	330	YML065W	279	2.6(10)-23	Saccharomyces cerevisiae	[ui:ym1065w] [pn:origin recognition complex, 104 kd subunit:origin recognition complex protein, subunit 1:origin recognition complex protein 120 kd subunit] [gn:orc1] [gtcf:10.1:10.2:10.8:12.8:12.9] [keggf:13.2] [sgdfc:3.3.0.3.6.0.4]
CONTIG1465	20008541_c3_8	5017	19120	669	223	YML060W	466	2.5(10)-44	Saccharomyces cerevisiae	[ui:ym1060w] [pn:8-oxoguanine dna glycosylase] [gn:ogg1:ym9958] [gtcf:10.1:10.10:10.2:14.1] [ec:3.2.2.-] [keggf:14.1] [sgdfc:9.5:0.11.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG275	3913128_c1_1	5018	19121	786	262	YML046W	102	0.00869	Saccharomyces cerevisiae	[ui:ym1046w] [pn:pre-mrna splicing factor:pre-mrna processing protein prp39] [gn:prp39:ym9827] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5049	25601563_f3_5	5019	19122	912	304	YML046W	105	0.0061	Saccharomyces cerevisiae	[ui:ym1046w] [pn:pre-mrna splicing factor:pre-mrna processing protein prp39] [gn:prp39:ym9827] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3214	1213380_f3_1	5020	19123	1710	570	YML043C	260	8.9(10)-20	Saccharomyces cerevisiae	[ui:ym1043c] [pn:rna polymerase i specific transcription initiation factor] [gn:rm11] [gtcf:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5467	23844680_f1_4	5021	19124	507	169	YML032C	164	2.1(10)-11	Saccharomyces cerevisiae	[ui:ym1032c] [pn:recombination and dna repair protein:dna repair and recombination protein] [gn:rad52] [gtcf:10.1:10.10.10.2:10.8:12.9] [keggfc:14.2] [sgdfc:3.3.0:3.7.0.9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5726	82_c1_17	5022	19125	1839	613	YML032C	485	4.9(10)-54	Saccharomyces cerevisiae	[ui:ym1032c] [pn:recombination and dna repair protein:dna repair and recombination protein] [gn:rad52] [gicfc:10.1:10.10.2:10.8:12.9] [keggfc:14.2] [sgdgc:3.3.0:3.7.0:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5467	33384427_c3_19	5023	19126	1029	343	YML031W	123	0.00012	Saccharomyces cerevisiae	[ui:ym1031w] [pn:nuclear envelope protein] [gn:ndc1] [gicfc:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3652	10243751_c3_3	5024	19127	651	217	YML027W	142	3.1(10)-9	Saccharomyces cerevisiae	[ui:ym1027w] [pn:homeodomain protein:homeobox protein] [gn:yox1] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5589	33150_f3_12	5025	19128	2799	933	YML010W	1134	4.0(10)-115	Saccharomyces cerevisiae	[ui:ym1010w] [pn:transcription initiation protein:transcription initiation protein spt5] [gn:spt5:ym9571] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8.1:4.8.3:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3572	26290937_f3_2	5026	19129	1056	352	YML007W	139	6.7(10)-14	Saccharomyces cerevisiae	[ui:ym1007w] [pn:transcriptional activator involved in oxidative stress response:transcriptional activator pdr4:yap-1 protein] [gn:pdr4:yap1:snq3:par1:ym9571] [gicfc:10.1:10.2:13.2] [keggfc:14.2] [sgdgc:4.8.2:9.5.0:11.1.0] [db:gtc-sac

CONTIG3590	21910777_f3_1	5027	19130	258	86	YML007W	212	2.2(10)-16	Saccharomyces cerevisiae	[ui:yml007w] [pn:transcriptional activator involved in oxidative stress response:transcriptional activator pdr4:yap-1 protein] [gn:pdr4:yap1:snq3:par1:ym9571] [gtcf:10.1:10.2:13.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0:11.1.0] [db:gtc-sac]
CONTIG5215	33750027_c3_14	5028	19131	543	181	YML007W	109	0.00083	Saccharomyces cerevisiae	[ui:yml007w] [pn:transcriptional activator involved in oxidative stress response:transcriptional activator pdr4:yap-1 protein] [gn:pdr4:yap1:snq3:par1:ym9571] [gtcf:10.1:10.2:13.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0:11.1.0] [db:gtc-sac]
CONTIG1922	33254630_f2_2	5029	19132	1002	334	YMR016C	516	3.2(10)-49	Saccharomyces cerevisiae	[ui:ymr016c] [pn:regulatory protein in the pka signal transduction pathway:sok2 protein] [gn:sok2:ym9711] [gtcf:12.13] [keggf:14.2] [sgdfc:3.2.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5673	6331442_f1_1	5030	19133	480	160	YMR039C	171	8.0(10)-13	Saccharomyces cerevisiae	[ui:ymr039c] [pn:transcriptional coactivator:sub1 protein] [gn:sub1:ym9532] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4526	23906250_c1_7	5031	19134	1914	638	YMR047C	299	1.3(10)-35	Saccharomyces cerevisiae	[ui:ymr047c] [pn:nuclear pore protein:nucleoporin nup116/nsp116:nuclear pore protein nup116/nsp116] [gn:nup116:nsp116:ym9532] [gtcf:10.1:10.2:10.6] [keggf:14.2] [sgdfc:4.5.0:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5667	34410090_f1_3	5032	19135	1344	448	YMR047C	199	2.1(10)-17	Saccharomyces cerevisiae	[ui:ymr047c] [pn:nuclear pore protein:nucleoporin nup116/nsp116:nuclear pore protein nup116/nsp116] [gn:nup116:nsp116:ym9532] [gtcf:10.1:10.2:10.6] [keggf:14.2] [sgdfc:4.5.0:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4321	21657628_c2_9	5033	19136	2076	692	YMR061W	572	1.8(10)-70	Saccharomyces cerevisiae	[ui:ymr061w] [pn:component of pre-mrna 3'-end processing factor cf:i:mrna 3'-end processing protein rna14] [gn:ma14:ym9796] [gtcf:10.1:10.2:10.9] [keggf:14.2] [sgdfc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5784	26285905_f2_5	5034	19137	2346	782	YMR078C	258	2.2(10)-38	Saccharomyces cerevisiae	[ui:ymr078c] [pn:required for accurate chromosome translocation in mitosis and maintenance of normal telomere length:chl12 protein] [gn:chl12:cf18:ym9582] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5784	24010800_f3_9	5035	19138	312	104	YMR078C	165	3.0(10)-11	Saccharomyces cerevisiae	[ui:yml078c] [pn:required for accurate chromosome transmission in mitosis and maintenance of normal telomere length:chl12 protein] [gn:chl12:efl8:ym9582] [gtcf:10.1:10.2:12.8] [keggc:14.2] [sgdfc:3.8:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5813	30209777_f3_31	5036	19139	1596	532	YMR106C	181	1.2(10)-10	Saccharomyces cerevisiae	[ui:yml106c] [pn:component of dna end-joining repair pathway] [gn:hdf2] [gtcf:10.1:10.2:10.8] [keggc:14.2] [sgdfc:3.7:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1251	35589436_f2_1	5037	19140	1236	412	YMR129W	269	7.5(10)-21	Saccharomyces cerevisiae	[ui:yml129w] [pn:nuclear pore membrane glycoprotein:nuclear envelope pore membrane protein pom152:p150] [gn:pom152:ym9553] [gtcf:10.1:10.2] [keggc:14.2] [sgdfc:8.1:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1780	10426006_f2_2	5038	19141	792	264	YMR129W	280	3.6(10)-23	Saccharomyces cerevisiae	[ui:yml129w] [pn:nuclear pore membrane glycoprotein:nuclear envelope pore membrane protein pom152:p150] [gn:pom152:ym9553] [gtcf:10.1:10.2] [keggc:14.2] [sgdfc:8.1:0.9:5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3661	161018_c3_5	5039	19142	273	91	YMR129W	225	2.6(10)-17	Saccharomyces cerevisiae	[ui:ymr129w] [pn:nuclear pore membrane glycoprotein:nuclear envelope pore membrane protein pom152:p150] [gn:pom152:ym9553] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2419	26455011_f1_2	5040	19143	1257	419	YMR137C	121	9.0(10)-17	Saccharomyces cerevisiae	[ui:ymr137c] [pn:dna repair protein] [gn:ps02] [gtcf:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5566	24414092_f2_11	5041	19144	1677	559	YMR137C	129	6.9(10)-5	Saccharomyces cerevisiae	[ui:ymr137c] [pn:dna repair protein] [gn:ps02] [gtcf:10.1:10.10:10.2] [keggfc:14.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1457	6834800_c3_1	5042	19145	549	183	YMR167W	340	5.0(10)-30	Saccharomyces cerevisiae	[ui:ymr167w] [pn:dna mismatch repair protein:mutl protein homolog l:dna mismatch repair protein mlh1] [gn:mlh1:ym8520] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2822	24428937_c3_1	5043	19146	1221	407	YMR167W	375	6.0(10)-50	Saccharomyces cerevisiae	[ui:ymr167w] [pn:dna mismatch repair protein:mutl protein homolog l:dna mismatch repair protein mlh1] [gn:mlh1:ym8520] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3961	21917137_f2_2	5044	19147	735	245	YMR167W	670	6.0(10)-66	Saccharomyces cerevisiae	[ui:ymr167w] [pn:dna mismatch repair protein:mutl protein homolog l:dna mismatch repair protein mlh1] [gn:mlh1:ym8520] [gtcf:10.1:10.2:10.8] [keggf:14.2] [sgdfc:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4228	12540775_c3_11	5045	19148	654	218	YMR167W	297	2.2(10)-25	Saccharomyces cerevisiae	[ui:ymr167w] [pn:dna mismatch repair protein:mutl protein homolog l:dna mismatch repair protein mlh1] [gn:mlh1:ym8520] [gtcf:10.1:10.2:10.8] [keggf:14.2] [sgdfc:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5344	6027165_f1_4	5046	19149	684	228	YMR197C	333	3.1(10)-30	Saccharomyces cerevisiae	[ui:ymr197c] [pn:similarity to nuf1p] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5111	16838411_c1_13	5047	19150	1197	399	YMR201C	564	3.3(10)-59	Saccharomyces cerevisiae	[ui:ymr201c] [pn:nucleotide excision repair protein:dna repair protein rad14] [gn:rad14:ym8325] [gtcf:10.1:10.10:10.2] [keggf:14.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4328	24883563_c1_3	5048	19151	810	270	YMR224C	782	8.0(10)-78	Saccharomyces cerevisiae	[ui:ymr224c] [pn:dna repair and meiotic recombination protein:mre11 protein] [gn:mre11:ym9959] [gtcf:10.1:10.2:10.8:12.8] [keggf:14.2] [sgdfc:3.5.0:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG648	4885950_c2_5	5049	19152	717	239	YMR224C	108	3.5(10)-5	Saccharomyces cerevisiae	[ui:ymr224c] [pn:dna repair and meiotic recombination protein:mre11 protein] [gn:mre11:ym9959] [gtcf:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5:0:3.7:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG648	15801542_c1_4	5050	19153	246	82	YMR224C	156	2.5(10)-10	Saccharomyces cerevisiae	[ui:ymr224c] [pn:dna repair and meiotic recombination protein:mre11 protein] [gn:mre11:ym9959] [gtcf:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5:0:3.7:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5817	24807938_c3_63	5051	19154	5262	1754	YMR229C	2455	0	Saccharomyces cerevisiae	[ui:ymr229c] [pn:processing of pre-ribosomal rna] [gn:rrp5] [gtcf:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.2:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5046	32087818_f2_2	5052	19155	255	85	YMR240C	156	1.2(10)-10	Saccharomyces cerevisiae	[ui:ymr240c] [pn:u2 snmp protein] [gn:cus1] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5046	26620138_f3_3	5053	19156	804	268	YMR240C	178	4.7(10)-13	Saccharomyces cerevisiae	[ui:ymr240c] [pn:u2 snmp protein] [gn:cus1] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.9:0:9.5:0] [db:gtc-saccharomyces cerevisiae]

CONTIG3657	24413880_c1_3	5054	19157	1824	608	YMR239C	449	1.6(10)-42	Saccharomyces cerevisiae	[ui:ymr239c] [pn:double-stranded ribonuclease] [gn:mt1] [gtcf:10.1:10.2:10.3] [keggfc:14.2] [sgdgc:4.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5748	21692010_f3_10	5055	19158	2049	683	YMR239C	160	1.8(10)-8	Saccharomyces cerevisiae	[ui:ymr239c] [pn:double-stranded ribonuclease] [gn:mt1] [gtcf:10.1:10.2:10.3] [keggfc:14.2] [sgdgc:4.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5739	21914553_f1_6	5056	19159	2889	963	YMR268C	281	1.0(10)-21	Saccharomyces cerevisiae	[ui:ymr268c] [pn:pre-mrna splicing factor:u4/u6 snrna-associated protein] [gn:prp24:ym8156] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5322	10975930_f1_2	5057	19160	1026	342	YMR276W	570	2.3(10)-55	Saccharomyces cerevisiae	[ui:ymr276w] [pn:ubiquitin-like protein:ubiquitin-like protein dsk2] [gn:dsk2:she4:ym8021] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5482	1365936_f3_13	5058	19161	2466	822	YMR284W	144	1.2(10)-25	Saccharomyces cerevisiae	[ui:ymr284w] [pn:high-affinity dna-binding protein:high affinity dna-binding factor subunit 1:ku70 homolog] [gn:hdf1:nes24:yku70:ym8021] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdgc:3.6.0:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5428	2432827_c1_12	5059	19162	564	188	YNL330C	117	2.0(10)-6	Saccharomyces cerevisiae	[ui:ynl330c] [pn:transcription modifier protein:histone deacetylase:transcriptional regulatory protein rpd3] [gn:rp3:sd12:n0305] [gtcf:10.1:10.2:12.15:12.9:13.10] [keggfc:14.2] [sgdfe:1.4.1:3.0:3.4.0:4.8.2:9.5.0] [db:gtc-saccharom]
CONTIG5428	390932_c3_17	5060	19163	1347	449	YNL330C	1756	5.0(10)-181	Saccharomyces cerevisiae	[ui:ynl330c] [pn:transcription modifier protein:histone deacetylase:transcriptional regulatory protein rpd3] [gn:rp3:sd12:n0305] [gtcf:10.1:10.2:12.15:12.9:13.10] [keggfc:14.2] [sgdfe:1.4.1:3.0:3.4.0:4.8.2:9.5.0] [db:gtc-saccharom]
CONTIG5485	24492127_f3_6	5061	19164	1524	508	YNL330C	1678	9.0(10)-173	Saccharomyces cerevisiae	[ui:ynl330c] [pn:transcription modifier protein:histone deacetylase:transcriptional regulatory protein rpd3] [gn:rp3:sd12:n0305] [gtcf:10.1:10.2:12.15:12.9:13.10] [keggfc:14.2] [sgdfe:1.4.1:3.0:3.4.0:4.8.2:9.5.0] [db:gtc-saccharom]
CONTIG4245	21745192_f2_3	5062	19165	543	181	YNL312W	254	7.2(10)-22	Saccharomyces cerevisiae	[ui:ynl312w] [pn:dna replication factor a, 36 kda subunit:replication factor-a protein 2:rf-a:dna binding protein buf1] [gn:rf2:buf1:n0368] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdfe:3.6.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4341	9851567_f2_2	5063	19166	1098	366	YNL290W	1044	1.3(10)-105	Saccharomyces cerevisiae	[ui:ynl290w] [pn:dna replication factor c, 40 kda subunit:activator 1 40 kd subunit:replication factor c 40 kd subunit] [gn:rfc3:n0533] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5417	24407812_f1_2	5064	19167	765	255	YNL282W	159	8.4(10)-12	Saccharomyces cerevisiae	[ui:ynl282w] [pn:involved in processing of tmas and rmas:hypothetical 22.6 kd protein in mrp10-erg24 intergenic region] [gn:pop3:n0586] [gtcf:10.1:10.2:10.3:10.6] [keggfc:14.2] [sgdfc:4.2:0.4:5.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2384	36117188_f2_2	5065	19168	573	191	YNL261W	113	1.6(10)-9	Saccharomyces cerevisiae	[ui:ynl261w] [pn:origin recognition complex, 50 kda subunit:origin recognition complex protein, subunit 5:origin recognition complex protein 53 kd subunit] [gn:orc5:n0834] [gtcf:10.1:10.2:10.8:12.8:12.9] [keggfc:13.2] [sgdfc:3.3:0.3]
CONTIG5793	4898311_c3_24	5066	19169	2073	691	YNL251C	628	3.7(10)-80	Saccharomyces cerevisiae	[ui:ynl251c] [pn:involved in regulation of nuclear pre-mrna abundance:nrd1 protein] [gn:nrd1:n0868] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8:2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1211	16282280_f3_1	5067	19170	609	203	YNL250W	159	2.7(10)-10	Saccharomyces cerevisiae	[ui:ynl250w] [pn:dna repair protein:dna repair protein rad50:153 kd protein] [gn:rad50:n0872] [gtcf:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5:0.3:7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2192	797518_c2_2	5068	19171	723	241	YNL250W	604	8.6(10)-58	Saccharomyces cerevisiae	[ui:ynl250w] [pn:dna repair protein:dna repair protein rad50:153 kd protein] [gn:rad50:n0872] [gtcf:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5:0.3:7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4056	9788502_f1_1	5069	19172	1038	346	YNL250W	103	0.03599	Saccharomyces cerevisiae	[ui:ynl250w] [pn:dna repair protein:dna repair protein rad50:153 kd protein] [gn:rad50:n0872] [gtcf:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5:0.3:7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5341	24854706_c1_14	5070	19173	1335	445	YNL250W	891	7.0(10)-89	Saccharomyces cerevisiae	[ui:ynl250w] [pn:dna repair protein:dna repair protein rad50:153 kd protein] [gn:rad50:n0872] [gtcf:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdfc:3.5:0.3:7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

b1x11175.y	11194187_f3_1	5071	19174	279	93	YNL250W	118	6.4(10)-6	Saccharomyces cerevisiae	[ui:ynl250w] [pn:dna repair protein:dna repair protein rad50:153 kd protein] [gn:rad50:n0872] [gtcf:10.1:10.2:10.8:12.8] [keggf:14.2] [sgdfc:3.5:0.3:7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4568	24804628_c1_6	5072	19175	1008	336	YNL236W	119	0.00038	Saccharomyces cerevisiae	[ui:ynl236w] [pn:global regulator protein:global transcriptional regulator sin4] [gn:sin4:tsf3:bel2:gal22:ssf5:n1135] [gtcf:10.1:10.2:12.13:12.15:12.9] [keggf:14.2] [sgdfc:1.1:2:1.5:2.3:3.0:3.4:0.4:8.2:9.5.0] [db:gtc-saccharomyces c
CONTIG4979	3990636_f2_5	5073	19176	732	244	YNL222W	544	1.5(10)-58	Saccharomyces cerevisiae	[ui:ynl222w] [pn:suppressor of cs mutant of sua7:ssu72 protein] [gn:ssu72:n1279] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8:2:9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4979	2922250_f2_6	5074	19177	897	299	YNL221C	442	7.0(10)-41	Saccharomyces cerevisiae	[ui:ynl221c] [pn:protein component of ribonuclease p and ribonuclease mrp:pop1 protein] [gn:pop1:n1285] [gtcf:10.1:10.2:10.3:10.6] [keggf:14.2] [sgdfc:4.2:0.4:5.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2176	11844207_f1_1	5075	19178	723	241	YNL206C	220	1.3(10)-17	Saccharomyces cerevisiae	[ui:ynl206c] [pn:similarity to structure-specific recognition proteins:hypothetical 51.6 kd protein in ssb2-spx18 intergenic region] [gn:n1346] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:9.5:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4506	2007662_c3_16	5076	19179	1671	557	YNL189W	1978	1.5(10)-204	Saccharomyces cerevisiae	[ui:ynl189w] [pn:karyopherin-alpha or importin:importin alpha subunit:karyopherin alpha subunit:serine-rich mna polymerase i suppressor protein] [gn:srp1:kap60:n1606] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.8:0.8.1:0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3708	4688950_c2_8	5077	19180	1695	565	YNL172W	617	7.0(10)-79	Saccharomyces cerevisiae	[ui:ynl172w] [pn:subunit of anaphase-promoting complex:cyclosome:hypothetical 196.1 kd protein in rps3-psd1 intergenic region] [gn:apcl:n1677] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.8:0.9:5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3902	23914011_f2_2	5078	19181	708	236	YNL167C	93	8.0(10)-5	Saccharomyces cerevisiae	[ui:ynl167c] [pn:cre-binding bzip protein:cre-binding bzip protein sko1] [gn:sko1:acr1:n1702] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8:2.9:5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4103	35303_f2_2	5079	19182	1611	537	YNL126W	583	1.6(10)-56	Saccharomyces cerevisiae	[ui:ynl126w] [pn:spindle pole body component:spc98] [gn:spc98:n1222:n1879] [gtcf:10.1:10.2:11.1:12.16:12.8] [keggfc:14.2] [sgdfc:3.8:0:9.1:0:9.2:0:9.3:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG3467	325_c3_3	5080	19183	396	132	YNL112W	250	1.2(10)-20	Saccharomyces cerevisiae	[ui:ynl112w] [pn:atp-dependent ma helicase of dead box family:p68-like protein] [gn:dbp2:n1945] [gtcf:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.2:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4462	860660_c3_4	5081	19184	1377	459	YNL112W	1556	7.7(10)-160	Saccharomyces cerevisiae	[ui:ynl112w] [pn:atp-dependent ma helicase of dead box family:p68-like protein] [gn:dbp2:n1945] [gtcf:10.1:10.2:10.3] [keggfc:14.2] [sgdfc:4.2:0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG2968	10329700_c2_3	5082	19185	1374	458	YNL088W	1270	1.6(10)-129	Saccharomyces cerevisiae	[ui:ynl088w] [pn:atp-hydrolysing:dna topoisomerase ii] [gn:top2:tor3:n2244] [gtcf:10.1:10.2:10.8:14.1] [ec:5.99.1.3] [keggfc:14.1] [sgdfc:3.6:0:3.7:0:9.5:0] [db:gtc-saccharomyces cerevisiae]

b3x14031.y	19962524_c1_2	5083	19186	486	162	YNL088W	506	3.2(10)-47	Saccharomyces cerevisiae	[ui:ynl088w] [pn:atp-hydrolysing:dna topoisomerase ii] [gn:top2:tor3:n2244] [gtcf:10.1:10.2:10.8:14.1] [ec:5.99.1.3] [keggfc:14.1] [sgdgc:3.6.0:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1244	953127_f2_2	5084	19187	999	333	YNL068C	429	3.3(10)-60	Saccharomyces cerevisiae	[ui:ynl068c] [pn:homology to d.melanogaster forkhead protein:fork head protein homolog 2] [gn:fkf2:n2403:ynl2403c] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3621	18813_c3_5	5085	19188	1560	520	YNL061W	1727	5.9(10)-178	Saccharomyces cerevisiae	[ui:ynl061w] [pn:nucleolar protein:nucleolar protein nop2] [gn:nop2:ynal:n2428:ynl2428w] [gtcf:10.1] [keggfc:14.2] [sgdgc:9.5.0:13.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5691	19723308_f2_11	5086	19189	363	121	YNL059C	111	1.8(10)-5	Saccharomyces cerevisiae	[ui:ynl059c] [pn:actin-related protein:hypothetical 87.6 kd protein in nop2-omp2 intergenic region] [gn:arp5:n2430:ynl2430c] [gtcf:10.1:10.2:12.16] [keggfc:14.2] [sgdgc:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5691	10335462_f3_18	5087	19190	1797	599	YNL059C	884	1.3(10)-88	Saccharomyces cerevisiae	[ui:ynl059c] [pn:actin-related protein:hypothetical 87.6 kd protein in nop2-omp2 intergenic region] [gn:arp5:n2430:ynl2430c] [gtcf:10.1:10.2:12.16] [keggfc:14.2] [sgdgc:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3388	13876567_f3_3	5088	19191	1929	643	YNL039W	507	1.1(10)-48	Saccharomyces cerevisiae	[ui:ynl039w] [pn:tftiib subunit, 90 kd:transcription factor tftiib b] [gn:tfc5:tfc7:n2682] [gtcf:10.1:10.2:10.3] [keggfc:14.2] [sgdgc:4.1.0.4.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4101	22520752_c2_7	5089	19192	1431	477	YNL025C	593	3.6(10)-67	Saccharomyces cerevisiae	[ui:ynl025c] [pn:dna-directed ma polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit, cyclin c homolog:ma polymerase ii holoenzyme cyclin-like subunit] [gn:ume3:ssn8:srb11:n2805] [gtcf:10.1:10.2:12.13:12.8] [keg
CONTIG3012	6672175_c3_6	5090	19193	489	163	YNL016W	145	2.0(10)-9	Saccharomyces cerevisiae	[ui:ynl016w] [pn:major polyadenylated ma-binding protein of nucleus and cytoplasm:nuclear and cytoplasmic polyadenylated ma-binding protein pub1:ars consensus binding protein acbp-60:poly:u-binding protein:poly uridylylate-binding pro
CONTIG5129	6642127_f3_6	5091	19194	1557	519	YNL016W	479	2.2(10)-76	Saccharomyces cerevisiae	[ui:ynl016w] [pn:major polyadenylated ma-binding protein of nucleus and cytoplasm:nuclear and cytoplasmic polyadenylated ma-binding protein pub1:ars consensus binding protein acbp-60:poly:u-binding protein:poly uridylylate-binding pro

CONTIG3755	4532762_f2_4	5092	19195	1044	348	YNL007C	538	5.0(10)-87	Saccharomyces cerevisiae	[ui:ynl007c] [pn:heat shock protein:sis1 protein] [gn:sis1:n2879] [gtcf:12.7:12.8] [keggfc:14.2] [sgdfc:3.8.0:5.2.0:9.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2372	961003_f3_1	5093	19196	1341	447	YNR011C	1108	2.2(10)-112	Saccharomyces cerevisiae	[ui:ynr011c] [pn:rna-dependent atpase of deah box family:pre-mrna splicing factor ma helicase prp2] [gn:prp2:ma2:n2048] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4666	4190937_c1_11	5094	19197	327	109	YNR011C	96	0.00088	Saccharomyces cerevisiae	[ui:ynr011c] [pn:rna-dependent atpase of deah box family:pre-mrna splicing factor ma helicase prp2] [gn:prp2:ma2:n2048] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3881	4860936_c3_7	5095	19198	1314	438	YNR023W	196	2.1(10)-23	Saccharomyces cerevisiae	[ui:ynr023w] [pn:component of swi/snf global transcription activator complex:transcription regulatory protein swp73:swi/snf complex component swp73] [gn:snf12:swp73:n3224] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-sa
CONTIG1850	35782_c3_10	5096	19199	1281	427	YNR052C	464	4.0(10)-44	Saccharomyces cerevisiae	[ui:ynr052c] [pn:required for glucose derepression:pop2 protein] [gn:pop2:caf1:n3470] [gtcf:10.1:10.2:12.13:12.15] [keggfc:14.2] [sgdfc:1.5.2:3.4.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5585	24647191_f3_14	5097	19200	1485	495	YNR052C	469	1.2(10)-44	Saccharomyces cerevisiae	[ui:ynr052c] [pn:required for glucose derepression:pop2 protein] [gn:pop2:caf1:n3470] [gtcf:10.1:10.2:12.13:12.15] [keggfc:14.2] [sgdgc:1.5.2:3.4.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3896	4020011_f2_3	5098	19201	1599	533	YOL148C	187	9.0(10)-26	Saccharomyces cerevisiae	[ui:yol148c] [pn:member of the tbp class of spt proteins that alter transcription site selection:transcription factor spt20] [gn:spt20:ada5] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5521	2822177_f1_3	5099	19202	1461	487	YOL123W	570	2.3(10)-55	Saccharomyces cerevisiae	[ui:yol123w] [pn:polyadenylated rna-binding protein] [gn:hrp1] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:9.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4742	12676553_f3_6	5100	19203	408	136	YOL116W	130	6.0(10)-8	Saccharomyces cerevisiae	[ui:yol116w] [pn:transcriptional activator:msn1 protein:multicopy suppressor of snf1 protein 1] [gn:msn1:fup1:phd2:hrb382] [gtcf:10.1:10.2:12.13] [keggfc:14.2] [sgdgc:1.5.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5328	10947055_c3_16	5101	19204	1809	603	YOL116W	177	8.0(10)-11	Saccharomyces cerevisiae	[ui:yol116w] [pn:transcriptional activator:msn1 protein:multicopy suppressor of snf1 protein 1] [gn:msn1:fup1:phd2:hrb382] [gtcf:10.1:10.2:12.13] [keggfc:14.2] [sgdgc:1.5.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5732	36367807_c2_29	5102	19205	1818	606	YOL115W	1140	9.4(10)-116	Saccharomyces cerevisiae	[ui:yol115w] [pn:topoisomerase i-related protein:topoisomerase 1-related protein trf4] [gn:trf4:o0716:hrc584] [gtcf:10.1:10.2:10.8:12.8] [keggfc:14.2] [sgdgc:3.6.0:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5417	22064657_f3_7	5103	19206	987	329	YOL094C	1137	1.8(10)-115	Saccharomyces cerevisiae	[ui:yol094c] [pn:dna replication factor c, 37 kda subunit:activator 1 37 kd subunit:replication factor c 37 kd subunit] [gn:rfc4:o0923] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdgc:3.6.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5651	9960027_f1_1	5104	19207	2604	868	YOL090W	1279	8.1(10)-168	Saccharomyces cerevisiae	[ui:yol090w] [pn:dna mismatch repair protein:muts protein homolog 2] [gn:msh2:o0935] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdgc:3.7.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5552	3939000_f1_1	5105	19208	1698	566	YOL089C	129	7.4(10)-7	Saccharomyces cerevisiae	[ui:yol089c] [pn:weak similarity to transcription factors] [gtcf:10.1:10.2] [keggfc:14.2] [sgdgc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5592	14275302_c3_8	5106	19209	2271	757	YOL089C	139	3.8(10)-11	Saccharomyces cerevisiae	[ui:yol089c] [pn:weak similarity to transcription factors] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
b2x16250.x	44824218_f1_1	5107	19210	747	249	YOL089C	91	0.34	Saccharomyces cerevisiae	[ui:yol089c] [pn:weak similarity to transcription factors] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1152	565875_f2_3	5108	19211	204	68	YOL069W	90	0.00169	Saccharomyces cerevisiae	[ui:yol069w] [pn:spindle pole body protein:myosin-like protein:nuclear filament-containing protein 2:nuclear division protein nuf2] [gn:nuf2] [gtcf:10.1:10.2:12.16:12.8] [keggf:14.2] [sgdfc:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces c
CONTIG1539	5911599_c1_3	5109	19212	954	318	YOL069W	198	1.7(10)-13	Saccharomyces cerevisiae	[ui:yol069w] [pn:spindle pole body protein:myosin-like protein:nuclear filament-containing protein 2:nuclear division protein nuf2] [gn:nuf2] [gtcf:10.1:10.2:12.16:12.8] [keggf:14.2] [sgdfc:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces c

CONTIG4978	14242151_fl_2	5110	19213	855	285	YOL067C	246	5.0(10)-21	Saccharomyces cerevisiae	[ui:yol067c] [pn:basic helix-loop-helix transcription factor that regulates cit2 gene expression:retrograde regulation protein 1] [gn:rig1] [gtcf:10.1:10.2:12.13] [keggc:14.2] [sgdfc:1.5.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1411	9806442_f2_2	5111	19214	816	272	YOL051W	166	3.8(10)-11	Saccharomyces cerevisiae	[ui:yol051w] [pn:dna-directed mat polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit:transcription regulatory protein gal11] [gn:gal11:spt13:rar3] [gtcf:10.1:10.2:12.13:12.15:12.9] [keggc:14.2] [sgdfc:1.5.2:3.3.]
CONTIG1537	25421931_c3_8	5112	19215	1317	439	YOL051W	108	7.5(10)-6	Saccharomyces cerevisiae	[ui:yol051w] [pn:dna-directed mat polymerase ii holoenzyme and kornberg's mediator:srb subcomplex subunit:transcription regulatory protein gal11] [gn:gal11:spt13:rar3] [gtcf:10.1:10.2:12.13:12.15:12.9] [keggc:14.2] [sgdfc:1.5.2:3.3.]
CONTIG1631	24023431_fl_2	5113	19216	1371	457	YOL006C	798	1.6(10)-79	Saccharomyces cerevisiae	[ui:yol006c] [pn:dna topoisomerase ii] [gn:top1:mak1] [gtcf:10.1:10.2:10.8:14.1] [ec:5.99.1.2] [keggc:14.1] [sgdfc:3.6.0:3.7.0:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG1633	20484390_c3_3	5114	19217	306	102	YOL004W	336	4.7(10)-29	Saccharomyces cerevisiae	[ui:yo1004w] [pn:transcription regulatory protein:paired amphipathic helix protein] [gn:sin3:sd1:ume4:rdp1:gam2] [gicfc:10.1:10.2:12.15:12.8:12.9] [keggfc:13.1] [sgdgc:1.6.4:3.3.0:3.4.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1633	975750_fl_1	5115	19218	564	188	YOL004W	710	5.9(10)-69	Saccharomyces cerevisiae	[ui:yo1004w] [pn:transcription regulatory protein:paired amphipathic helix protein] [gn:sin3:sd1:ume4:rdp1:gam2] [gicfc:10.1:10.2:12.15:12.8:12.9] [keggfc:13.1] [sgdgc:1.6.4:3.3.0:3.4.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2942	14117288_fl_1	5116	19219	1086	362	YOL004W	581	3.6(10)-55	Saccharomyces cerevisiae	[ui:yo1004w] [pn:transcription regulatory protein:paired amphipathic helix protein] [gn:sin3:sd1:ume4:rdp1:gam2] [gicfc:10.1:10.2:12.15:12.8:12.9] [keggfc:13.1] [sgdgc:1.6.4:3.3.0:3.4.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2942	30080143_f2_3	5117	19220	738	246	YOL004W	225	3.2(10)-17	Saccharomyces cerevisiae	[ui:yol004w] [pn:transcription regulatory protein:paired amphipathic helix protein] [gn:sin3:sdi1:ume4:rdp1:gam2] [gtcf:10.1:10.2:12.15:12.8:12.9] [keggfc:13.1] [sgdfc:1.6.4:3.3.0:3.4.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4369	13679061_c1_7	5118	19221	945	315	YOL004W	288	3.2(10)-41	Saccharomyces cerevisiae	[ui:yol004w] [pn:transcription regulatory protein:paired amphipathic helix protein] [gn:sin3:sdi1:ume4:rdp1:gam2] [gtcf:10.1:10.2:12.15:12.8:12.9] [keggfc:13.1] [sgdfc:1.6.4:3.3.0:3.4.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4369	25866430_c2_10	5119	19222	585	195	YOL004W	173	1.1(10)-11	Saccharomyces cerevisiae	[ui:yol004w] [pn:transcription regulatory protein:paired amphipathic helix protein] [gn:sin3:sdi1:ume4:rdp1:gam2] [gtcf:10.1:10.2:12.15:12.8:12.9] [keggfc:13.1] [sgdfc:1.6.4:3.3.0:3.4.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2417	35188800_f3_2	5120	19223	771	257	YOL001W	288	1.8(10)-25	Saccharomyces cerevisiae	[ui:yol001w] [pn:cyclin:phosphate system cyclin pho80] [gn:pho80:tup7:o2505:unb293] [gtcf:10.1:10.2:12.8:13.10] [keggfc:13.2] [sgdfc:1.4.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4252	23832562_c1_7	5121	19224	2676	892	YOR038C	631	1.3(10)-80	Saccharomyces cerevisiae	[ui:yor038c] [pn:histone transcription regulator:histone transcription regulator 2] [gn:hir2:or26] [gdcf:10.1:10.2] [keggf:14.2] [sgdcf:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5125	817965_c2_13	5122	19225	321	107	YOR039W	135	6.5(10)-9	Saccharomyces cerevisiae	[ui:yor039w] [pn:casein kinase ii beta" chain:ck ii] [gn:ckb2:or26] [gdcf:10.1:10.2:12.13] [ec:2.7.1.37] [keggf:14.1] [sgdcf:4.7.0:9.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5125	16839061_c2_12	5123	19226	450	150	YOR039W	357	8.8(10)-33	Saccharomyces cerevisiae	[ui:yor039w] [pn:casein kinase ii beta" chain:ck ii] [gn:ckb2:or26] [gdcf:10.1:10.2:12.13] [ec:2.7.1.37] [keggf:14.1] [sgdcf:4.7.0:9.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1954	898453_c3_9	5124	19227	762	254	YOR048C	188	1.6(10)-13	Saccharomyces cerevisiae	[ui:yor048c] [pn:5"-3" exoribonuclease:ribonucleic acid trafficking protein 1] [gn:rat1:hkel:tap1] [gdcf:10.1:10.2:10.3:14.1] [ec:3.1.11.-] [keggf:14.1] [sgdcf:4.2.0:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3145	17032156_c3_5	5125	19228	549	183	YOR048C	395	1.2(10)-35	Saccharomyces cerevisiae	[ui:yor048c] [pn:5"-3" exoribonuclease:ribonucleic acid trafficking protein 1] [gn:rat1:hkel:tap1] [gdcf:10.1:10.2:10.3:14.1] [ec:3.1.11.-] [keggf:14.1] [sgdcf:4.2.0:8.1.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3505	191557_c1_4	5126	19229	513	171	YOR058C	130	2.1(10)-7	Saccharomyces cerevisiae	[ui:yor058c] [pn:microtubule-associated protein:nonmotor:anaphase spindle elongation protein] [gn:ase1] [gtcf:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4199	6024011_f3_2	5127	19230	1869	623	YOR058C	313	8.3(10)-25	Saccharomyces cerevisiae	[ui:yor058c] [pn:microtubule-associated protein:nonmotor:anaphase spindle elongation protein] [gn:ase1] [gtcf:10.1:10.2:12.16:12.8] [keggfc:14.2] [sgdfc:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5406	6646925_c2_11	5128	19231	1002	334	YOR061W	1148	1.3(10)-116	Saccharomyces cerevisiae	[ui:yor061w] [pn:casein kinase ii alpha" chain:casein kinase ii, alpha" chain:ck ii] [gn:cka2] [gtcf:10.1:10.2:12.13:12.8] [ec:2.7.1.37] [keggfc:14.1] [sgdfc:3.8.0:4.7.0:9.5.0:15.0.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4701	23925327_c1_5	5129	19232	1974	658	YOR113W	477	1.5(10)-54	Saccharomyces cerevisiae	[ui:yor113w] [pn:asparagine-rich zinc finger protein:asparagine-rich zinc finger protein azf1] [gn:azf1:o3244:yor3244w] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.12.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3490	4140650_f3_3	5130	19233	2097	699	YOR140W	239	3.0(10)-22	Saccharomyces cerevisiae	[ui:yor140w] [pn:transcription factor:flocculation suppression protein:sfl1 protein] [gn:sfl1:yor3339w] [gtcf:10.1:10.2] [keggc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4557	9925880_c1_5	5131	19234	1086	362	YOR140W	195	1.2(10)-19	Saccharomyces cerevisiae	[ui:yor140w] [pn:transcription factor:flocculation suppression protein:sfl1 protein] [gn:sfl1:yor3339w] [gtcf:10.1:10.2] [keggc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1476	1067693_f1_1	5132	19235	522	174	YOR194C	128	5.5(10)-8	Saccharomyces cerevisiae	[ui:yor194c] [pn:tfiia subunit:transcription initiation factor, 32 kd:transcription initiation factor iia large chain:tfiia 32 kd subunit] [gn:toa1] [gtcf:10.1:10.2] [keggc:14.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5758	14647127_c1_16	5133	19236	894	298	YOR194C	128	2.7(10)-18	Saccharomyces cerevisiae	[ui:yor194c] [pn:tfiia subunit:transcription initiation factor, 32 kd:transcription initiation factor iia large chain:tfiia 32 kd subunit] [gn:toa1] [gtcf:10.1:10.2] [keggc:14.2] [sgdfc:4.8.1:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5473	3947177_c1_7	5134	19237	222	74	YOR210W	313	4.0(10)-28	Saccharomyces cerevisiae	[ui:yor210w] [pn:dna-directed polymerase i, ii, iii 8.3 subunit:dna-directed rna polymerases i, ii, and iii 8.3 kd polypeptide:abc10-beta:abc8] [gn:rpb10] [gtcf:10.1:10.2:10.3] [keggf:14.2] [sgdf:4.1.0.4.0.4.8.1:9.5.0] [db:gtc-sa]
CONTIG4882	4867926_c2_9	5135	19238	1956	652	YOR217W	941	2.1(10)-128	Saccharomyces cerevisiae	[ui:yor217w] [pn:dna replication factor c, 95 kd subunit:activator 1 95 kd subunit:replication factor c 95 kd subunit:cell division control protein 44] [gn:rfc1:cdc44:yor50-7] [gtcf:10.1:10.2:10.8:12.8] [keggf:14.2] [sgdf:3.6.0:3.8]
CONTIG2108	26441302_f2_2	5136	19239	183	61	YOR257W	96	4.0(10)-5	Saccharomyces cerevisiae	[ui:yor257w] [pn:spindle pole body component, centrin:cell division control protein 31] [gn:cdc31:dsk1] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdf:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1967	32440881_c3_2	5137	19240	1044	348	YOR290C	118	0.0011	Saccharomyces cerevisiae	[ui:yor290c] [pn:component of swi/snf global transcription activator complex:transcription regulatory protein snf2:swi/snf complex component snf2:regulatory protein swi2:regulatory protein gam1:transcription factor tye3] [gn:snf2:swi2:

CONTIG4757	23672202_c3_7	5138	19241	861	287	YOR290C	313	1.6(10)-26	Saccharomyces cerevisiae	[ui:yor290c] [pn:component of swi/snf global transcription activator complex:transcription regulatory protein snf2:swi/snf complex component snf2:regulatory protein swi2:regulatory protein gam1:transcription factor tye3] [gn:snf2:swi2:
CONTIG5776	548153_f3_17	5139	19242	2940	980	YOR290C	1235	3.8(10)-129	Saccharomyces cerevisiae	[ui:yor290c] [pn:component of swi/snf global transcription activator complex:transcription regulatory protein snf2:swi/snf complex component snf2:regulatory protein swi2:regulatory protein gam1:transcription factor tye3] [gn:snf2:swi2:
CONTIG151	17037564_cl_1	5140	19243	588	196	YOR290C	745	1.3(10)-72	Saccharomyces cerevisiae	[ui:yor290c] [pn:component of swi/snf global transcription activator complex:transcription regulatory protein snf2:swi/snf complex component snf2:regulatory protein swi2:regulatory protein gam1:transcription factor tye3] [gn:snf2:swi2:

CONTIG1781	35283264_c1_3	5141	19244	678	226	YOR290C	659	2.1(10)-63	Saccharomyces cerevisiae	[ui:yor290c] [pn:component of swi/snf global transcription activator complex:transcription regulatory protein snf2:swi/snf complex component snf2:regulatory protein swi2:regulatory protein gam1:transcription factor tye3] [gn:snf2:swi2:
CONTIG3991	14095056_c2_9	5142	19245	807	269	YOR319W	393	1.3(10)-36	Saccharomyces cerevisiae	[ui:yor319w] [pn:similarity to human sap49 and ma-binding proteins] [gn:hsh49] [gtcf:10.1:10.2:10.9] [keggfc:14.2] [sgdfe:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1988	5250758_c2_2	5143	19246	1767	589	YOR337W	187	3.2(10)-11	Saccharomyces cerevisiae	[ui:yor337w] [pn:tyl enhancer activator] [gn:teal:o6257] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfe:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3818	23866327_c3_3	5144	19247	1383	461	YOR337W	460	4.9(10)-51	Saccharomyces cerevisiae	[ui:yor337w] [pn:tyl enhancer activator] [gn:teal:o6257] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfe:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4425	4797183_c1_9	5145	19248	822	274	YOR344C	209	4.2(10)-17	Saccharomyces cerevisiae	[ui:yor344c] [pn:basic helix-loop-helix transcription factor:serine-rich protein tye7:basic-helix-loop-helix protein sgc1] [gn:tye7:sgc1:o6233] [gtcf:10.1:10.2:12.13] [keggfc:14.2] [sgdfe:1.5.2:4.8.2:9.5.0] [db:gtc-saccharomyces cere

CONTIG5154	33787535_c2_14	5146	19249	1164	388	YOR358W	403	1.2(10)-37	Saccharomyces cerevisiae	[ui:yor358w] [pn:ccaat-binding factor subunit] [gn:hap5] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5815	12588150_fl_3	5147	19250	633	211	YPL248C	240	3.7(10)-19	Saccharomyces cerevisiae	[ui:ypl248c] [pn:transcription factor:regulatory protein] [gn:gal4] [gtcf:10.1:10.2:12.13] [keggf:14.2] [sgdfc:1.5.2:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2382	31275181_fl_1	5148	19251	1464	488	YPL190C	244	1.1(10)-17	Saccharomyces cerevisiae	[ui:ypl190c] [pn:polyadenylated rna-binding protein:nuclear polyadenylated rna-binding protein] [gn:nab3] [gtcf:10.1:10.2:10.9] [keggf:14.2] [sgdfc:4.10.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5737	15709528_f3_10	5149	19252	1086	362	YPL177C	191	4.7(10)-15	Saccharomyces cerevisiae	[ui:ypl177c] [pn:copper homeostasis protein:homeobox protein] [gn:cup9] [gtcf:10.1:10.2:12.6:12.8] [keggf:13.1] [sgdfc:1.8.1:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1448	1432316_fl_1	5150	19253	1518	506	YPL128C	265	8.4(10)-47	Saccharomyces cerevisiae	[ui:ypl128c] [pn:telomere tagg repeat-binding factor 1:tbfl protein:tagg repeat-binding factor 1:tbfl alpha] [gn:tbfl:tpi16c] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:9.5.0:9.6.0] [db:gtc-saccharomyces cerevisiae]

b1x18204.x	23484431_c1_3	5151	19254	786	262	YPL089C	240	9.5(10)-23	Saccharomyces cerevisiae	[ui:yp1089c] [pn:transcription factor of the mads box family] [gn:rlm1] [gtcf:10.1:10.2:12.13:12.8] [keggfc:14.2] [sgdfc:4.8.2:9.5.0:10.2.7] [db:gtc-saccharomyces cerevisiae]
CONTIG3080	34072192_f3_1	5152	19255	693	231	YPL082C	313	1.8(10)-26	Saccharomyces cerevisiae	[ui:yp1082c] [pn:transcriptional accessory protein:probable helicase mot1] [gn:mot1:lpf4c] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3375	12689587_c2_5	5153	19256	1887	629	YPL082C	1301	2.5(10)-132	Saccharomyces cerevisiae	[ui:yp1082c] [pn:transcriptional accessory protein:probable helicase mot1] [gn:mot1:lpf4c] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3509	31927007_f1_1	5154	19257	1662	554	YPL082C	1636	1.8(10)-179	Saccharomyces cerevisiae	[ui:yp1082c] [pn:transcriptional accessory protein:probable helicase mot1] [gn:mot1:lpf4c] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG800	19586568_f2_1	5155	19258	813	271	YPL082C	159	5.0(10)-9	Saccharomyces cerevisiae	[ui:yp1082c] [pn:transcriptional accessory protein:probable helicase mot1] [gn:mot1:lpf4c] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

b2x17437.y	22928188_c2_4	5156	19259	633	211	YPL082C	570	7.7(10)-54	Saccharomyces cerevisiae	[ui:yp1082c] [pn:transcriptional accessory protein:probable helicase motif] [gn:mot1:lpf4c] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4110	4017182_f3_3	5157	19260	2280	760	YPL043W	1153	2.2(10)-150	Saccharomyces cerevisiae	[ui:yp1043w] [pn:nucleolar protein:nucleolar protein nop4:nop4:nop77] [gn:nop4:nop77] [gtcf:10.1:10.2:10.3] [keggf:14.2] [sgdfc:4.2.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5317	9772711_c2_14	5158	19261	312	104	YPL022W	143	1.1(10)-8	Saccharomyces cerevisiae	[ui:yp1022w] [pn:component of the nucleotide excision repairosome:dna repair protein] [gn:rad1] [gtcf:10.1:10.10:10.2] [keggf:14.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5317	33789687_c2_13	5159	19262	2595	865	YPL022W	1059	3.6(10)-107	Saccharomyces cerevisiae	[ui:yp1022w] [pn:component of the nucleotide excision repairosome:dna repair protein] [gn:rad1] [gtcf:10.1:10.10:10.2] [keggf:14.2] [sgdfc:9.5.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3345	25478402_c1_7	5160	19263	1557	519	YPL016W	164	4.2(10)-13	Saccharomyces cerevisiae	[ui:yp1016w] [pn:component of swi/snf global transcription activator complex:transcription regulatory protein adr6:swi/snf complex component adr6:regulatory protein swi1:regulatory protein gam3] [gn:adr6:swi1:gam3] [gtcf:10.1:10.2:12.

CONTIG4649	4003906_c1_6	5161	19264	1470	490	YPL016W	186	7.0(10)-11	Saccharomyces cerevisiae	[ui:yp1016w] [pn:component of swi/snf global transcription activator complex:transcription regulatory protein adr6:swi/snf complex component adr6:regulatory protein swi1:regulatory protein gam3] [gn:adr6:swi1:gam3] [gtcf:10.1:10.2:12.2]
CONTIG4345	4710926_c2_9	5162	19265	813	271	YPL008W	277	4.0(10)-41	Saccharomyces cerevisiae	[ui:yp1008w] [pn:protein of the deah box family:chl1 protein] [gn:chl1:ctf1:yp8132] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4413	1054567_f2_1	5163	19266	1227	409	YPL008W	722	1.8(10)-71	Saccharomyces cerevisiae	[ui:yp1008w] [pn:protein of the deah box family:chl1 protein] [gn:chl1:ctf1:yp8132] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4413	26585900_f3_3	5164	19267	231	77	YPL008W	181	7.2(10)-13	Saccharomyces cerevisiae	[ui:yp1008w] [pn:protein of the deah box family:chl1 protein] [gn:chl1:ctf1:yp8132] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4413	23882316_f2_2	5165	19268	216	72	YPL008W	140	1.8(10)-8	Saccharomyces cerevisiae	[ui:yp1008w] [pn:protein of the deah box family:chl1 protein] [gn:chl1:ctf1:yp8132] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdgc:3.8.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5575	29495216_c1_11	5166	19269	1212	404	YPL001W	634	3.8(10)-62	Saccharomyces cerevisiae	[ui:yp1001w] [pn:histone acetyltransferase subunit] [gn:hat1] [gtcf:10.1:10.2:10.7] [keggf:14.2] [sgdf:6.3:0.9:2.0:9.5:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4598	4726387_f3_4	5167	19270	1125	375	YPR025C	466	2.5(10)-44	Saccharomyces cerevisiae	[ui:ypr025c] [pn:tfiih subunit:transcription initiation factor, cyclin c component:cyclin ccl1] [gn:ccl1:ypr024c:yp9367] [gtcf:10.1:10.10:10.2:12.8] [keggf:14.2] [sgdf:3.8:0.4:8.1:9.5:0:11.2:1] [db:gtc-saccharomyces cerevisiae]
CONTIG1927	24406550_c3_8	5168	19271	276	92	YPR052C	245	6.5(10)-21	Saccharomyces cerevisiae	[ui:ypr052c] [pn:nonhistone chromosomal protein related to mammalian hmg1:nonhistone chromosomal protein 6a] [gn:nhp6a:nhpa:yp9499] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdf:3.1:0.3:2.0:9.5:0:9.6:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5403	31875_c2_7	5169	19272	765	255	YPR057W	109	0.001	Saccharomyces cerevisiae	[ui:ypr057w] [pn:involved in snmp biogenesis] [gn:brt1] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:4.9:0.9:5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5251	167182_c3_19	5170	19273	1857	619	YPR065W	258	2.7(10)-22	Saccharomyces cerevisiae	[ui:ypr065w] [pn:heme-dependent transcriptional repressor of hypoxic genes:rox1 repressor:hypoxic function repressor:heme- dependent repression factor] [gn:rox1:yp9499] [gtcf:10.1:10.2:12.13:12.8] [keggf:13.1] [sgdf:1.7.3:4.8.2:9.5]
CONTIG5217	9960077_f3_8	5171	19274	426	142	YPR086W	339	7.0(10)-31	Saccharomyces cerevisiae	[ui:ypr086w] [pn:tfiib subunit:transcription initiation factor, factor e:transcription initiation factor iib:tfiib:transcription factor e] [gn:sua7:p9513] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:4.8.1:9.5.0] [db:gtc-saccharomyces cerev]
CONTIG5414	34187502_c3_9	5172	19275	564	188	YPR086W	316	1.8(10)-28	Saccharomyces cerevisiae	[ui:ypr086w] [pn:tfiib subunit:transcription initiation factor, factor e:transcription initiation factor iib:tfiib:transcription factor e] [gn:sua7:p9513] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:4.8.1:9.5.0] [db:gtc-saccharomyces cerev]
CONTIG5728	13705008_c2_18	5173	19276	1056	352	YPR086W	919	2.5(10)-92	Saccharomyces cerevisiae	[ui:ypr086w] [pn:tfiib subunit:transcription initiation factor, factor e:transcription initiation factor iib:tfiib:transcription factor e] [gn:sua7:p9513] [gtcf:10.1:10.2] [keggf:14.2] [sgdf:4.8.1:9.5.0] [db:gtc-saccharomyces cerev]

CONTIG4832	34410427_f3_3	5174	19277	3018	1006	YPR104C	363	1.2(10)-50	Saccharomyces cerevisiae	[ui:ypr104c] [pn:transcriptional activator of the forkhead/hnf3 fh11] [gn:fh11:p8283] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG952	11893830_f1_1	5175	19278	825	275	YPR104C	365	1.7(10)-32	Saccharomyces cerevisiae	[ui:ypr104c] [pn:transcriptional activator of the forkhead/hnf3 fh11] [gn:fh11:p8283] [gtcf:10.1:10.2] [keggfc:14.2] [sgdfc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5127	4382687_c3_9	5176	19279	2430	810	YPR135W	499	8.3(10)-75	Saccharomyces cerevisiae	[ui:ypr135w] [pn:dna-directed dna polymerase alpha-binding protein:dna polymerase alpha-binding protein:pob1/ctf4 protein:chromosome replication protein ch115] [gn:pob1:ctf4:ch115:p9659] [gtcf:10.1:10.2:10.8] [keggfc:14.2] [sgdfc:3.6]
CONTIG5789	5917193_f2_7	5177	19280	1002	334	YPR141C	882	2.0(10)-88	Saccharomyces cerevisiae	[ui:ypr141c] [pn:kinesin-related protein:kinesin-like protein kar3:nuclear fusion protein] [gn:kar3:p9659] [gtcf:10.1:10.2:12.16:12.8:12.9] [keggfc:14.2] [sgdfc:3.0:3.8.0:9.3.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3097	36047827_f3_1	5178	19281	513	171	YPR168W	306	2.2(10)-27	Saccharomyces cerevisiae	[ui:ypr168w] [pn:negative regulator of ho endonuclease] [gn:nut2] [gtcf:10.1:10.2:12.9] [keggf:14.2] [sgdf:3.3.0:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG393	25425906_c2_4	5179	19282	687	229	YPR162C	96	0.039	Saccharomyces cerevisiae	[ui:ypr162c] [pn:origin recognition complex, 56 kd subunit:origin recognition complex protein, subunit 3:origin recognition complex protein 56 kd subunit] [gn:orc4:p9325] [gtcf:10.1:10.2:10.8:12.8:12.9] [keggf:13.2] [sgdf:3.3.0:3.6]
CONTIG3767	26353552_c3_4	5180	19283	963	321	YPR178W	289	4.7(10)-45	Saccharomyces cerevisiae	[ui:ypr178w] [pn:u4/u6 snmp 52 kd protein:u4/u6 small nuclear ribonucleoprotein prp4] [gn:prp4:ma4:p9705] [gtcf:10.1:10.2:12.16] [keggf:14.2] [sgdf:4.9.0:6.4.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3767	22054712_c2_3	5181	19284	465	155	YPR178W	98	6.0(10)-8	Saccharomyces cerevisiae	[ui:ypr178w] [pn:u4/u6 snmp 52 kd protein:u4/u6 small nuclear ribonucleoprotein prp4] [gn:prp4:ma4:p9705] [gtcf:10.1:10.2:12.16] [keggf:14.2] [sgdf:4.9.0:6.4.0.9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG408	12671961_c1_4	5182	19285	378	126	YPR182W	215	9.8(10)-18	Saccharomyces cerevisiae	[ui:ypr182w] [pn:snrna-associated protein of the sm family:small nuclear ribonucleoprotein like protein smx3] [gn:smx3:p9705] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2830	6672151_fl_1	5183	19286	396	132	YPR182W	136	2.2(10)-9	Saccharomyces cerevisiae	[ui:ypr182w] [pn:snrna-associated protein of the sm family:small nuclear ribonucleoprotein like protein smx3] [gn:smx3:p9705] [gicfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.9.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2486	289003_c1_7	5184	19287	627	209	YPR186C	137	4.2(10)-14	Saccharomyces cerevisiae	[ui:ypr186c] [pn:transcription initiation factor:transcription factor iiia:tfiiia] [gn:tfc2:pzf1:tfiiia:p9677] [gicfc:10.1:10.2:10.3] [keggfc:14.2] [sgdgc:4.1.0:4.4.0:9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4935	21663962_c2_6	5185	19288	426	142	YPR186C	96	0.0014	Saccharomyces cerevisiae	[ui:ypr186c] [pn:transcription initiation factor:transcription factor iiia:tfiiia] [gn:tfc2:pzf1:tfiiia:p9677] [gicfc:10.1:10.2:10.3] [keggfc:14.2] [sgdgc:4.1.0:4.4.0:9.5.0] [db:gtc-saccharomyces cerevisiae]

b9x10d47.x	2557307_f2_1	5186	19289	462	154	YPR186C	357	8.8(10)-33	Saccharomyces cerevisiae	[ui:ypr186c] [pn:transcription initiation factor:transcription factor iiiia:tfiiiia] [gn:tfc2:pzf1:tfiiiia:p9677] [gtcfc:10.1:10.2:10.3] [keggfc:14.2] [sgdgc:4.1.0.4.0.9.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2145	25395386_f1_1	5187	19290	1092	364	YPR189W	94	0.28	Saccharomyces cerevisiae	[ui:ypr189w] [pn:antiviral protein:superkiller 3 protein] [gn:ski3] [gtcfc:10.1:10.2:12.14] [keggfc:14.2] [sgdgc:9.5.0:11.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5354	14645010_c2_9	5188	19291	2262	754	YPR189W	688	5.0(10)-101	Saccharomyces cerevisiae	[ui:ypr189w] [pn:antiviral protein:superkiller 3 protein] [gn:ski3] [gtcfc:10.1:10.2:12.14] [keggfc:14.2] [sgdgc:9.5.0:11.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4566	10642129_c1_3	5189	19292	1830	610	YPR189W	851	3.2(10)-84	Saccharomyces cerevisiae	[ui:ypr189w] [pn:antiviral protein:superkiller 3 protein] [gn:ski3] [gtcfc:10.1:10.2:12.14] [keggfc:14.2] [sgdgc:9.5.0:11.7.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1907	4484389_c1_2	5190	19293	1557	519	YPR196W	152	6.5(10)-8	Saccharomyces cerevisiae	[ui:ypr196w] [pn:strong similarity to regulatory protein mal63p:maltose fermentation regulatory protein mal6r] [gn:mal6r:mal63] [gtcfc:10.1:10.2] [keggfc:14.2] [sgdgc:4.8.2:9.5.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4799	35183443_cl_6	5191	19294	2370	790	YBL088C	131	2.1(10)-10	Saccharomyces cerevisiae	[ui:ybl088c] [pn:telomere length control protein:telomere length regulation protein tel1] [gn:tel1:ybl0706] [gdcf:10.1] [keggf:14.2] [sgdgc:9.6.0] [db:gdc-saccharomyces cerevisiae]
CONTIG4943	12594443_f3_1	5192	19295	2400	800	YBL088C	889	1.8(10)-87	Saccharomyces cerevisiae	[ui:ybl088c] [pn:telomere length control protein:telomere length regulation protein tel1] [gn:tel1:ybl0706] [gdcf:10.1] [keggf:14.2] [sgdgc:9.6.0] [db:gdc-saccharomyces cerevisiae]
CONTIG5480	19550937_f3_4	5193	19296	555	185	YBL088C	112	0.00209	Saccharomyces cerevisiae	[ui:ybl088c] [pn:telomere length control protein:telomere length regulation protein tel1] [gn:tel1:ybl0706] [gdcf:10.1] [keggf:14.2] [sgdgc:9.6.0] [db:gdc-saccharomyces cerevisiae]
CONTIG5480	10160093_f1_2	5194	19297	2844	948	YBL088C	108	0.00077	Saccharomyces cerevisiae	[ui:ybl088c] [pn:telomere length control protein:telomere length regulation protein tel1] [gn:tel1:ybl0706] [gdcf:10.1] [keggf:14.2] [sgdgc:9.6.0] [db:gdc-saccharomyces cerevisiae]
CONTIG5236	26564680_cl_8	5195	19298	1344	448	YBR195C	603	7.5(10)-59	Saccharomyces cerevisiae	[ui:ybr195c] [pn:chromatin assembly complex, subunit p50:msi1 protein:ira1 multicopy suppressor] [gn:msi1:ybr1405] [gdcf:10.1:10.2:10.8:12.13:12.16] [keggf:14.2] [sgdgc:3.6.0:4.8.3:6.4.0:9.6.0:10.4.5] [db:gdc-saccharomyces cerevisiae]

CONTIG5540	136887_f3_11	5196	19299	525	175	YDL208W	481	6.4(10)-46	Saccharomyces cerevisiae	[ui:ydl208w] [pn:strong similarity to high mobility group.hmg family:high mobility group-like nuclear protein 2] [gn:nhp2.d1045] [gtcf:10.1:10.4] [keggf:14.2] [sgdfc:5.1.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2920	32658177_f1_1	5197	19300	882	294	YDL002C	263	4.2(10)-30	Saccharomyces cerevisiae	[ui:ydl002c] [pn:non-histone protein] [gn:hmo2] [gtcf:10.1] [keggf:14.2] [sgdfc:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4371	10285206_c1_6	5198	19301	1203	401	YDR174W	141	8.5(10)-15	Saccharomyces cerevisiae	[ui:ydr174w] [pn:non-histone protein] [gn:hmo1] [gtcf:10.1] [keggf:14.2] [sgdfc:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5258	24242255_c3_12	5199	19302	402	134	YEL026W	505	1.8(10)-48	Saccharomyces cerevisiae	[ui:yel026w] [pn:strong similarity to high mobility group-like protein nhp2p:putative 60s ribosomal protein yel026w] [gtcf:10.1:10.4] [keggf:14.2] [sgdfc:5.1.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1876	19531250_c1_3	5200	19303	618	206	YER159C	249	2.3(10)-21	Saccharomyces cerevisiae	[ui:yer159c] [pn:functional homolog of human nc2alpha:hypothetical 15.5 kd protein in bem2-spt2 intergenic region] [gn:bur6] [gtcf:10.1:10.2] [keggf:14.2] [sgdfc:4.8.2:9.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5754	9804627_f3_15	5201	19304	1734	578	YFR037C	614	3.2(10)-75	Saccharomyces cerevisiae	[lui:yfr037c] [pn:subunit of the rsc complex:hypothetical 63.2 kd protein in cdc26-sap155 intergenic region] [gn:rsc8] [gtcf:10.1:10.2:12.8] [keggfc:14.2] [sgdfc:3.8:0.4:8.2:4.8:3:9.6:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4529	2775952_f1_3	5202	19305	1365	455	YGL194C	1506	1.5(10)-154	Saccharomyces cerevisiae	[lui:ygl194c] [pn:putative deacetylase:hypothetical 51.5 kd protein in gen1-spo8 intergenic region] [gn:rtl1:g1330] [gtcf:10.1:10.2:10.7] [keggfc:14.2] [sgdfc:4.8:3:6.3:0.9:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5809	23834450_c1_16	5203	19306	1164	388	YGL194C	398	4.0(10)-37	Saccharomyces cerevisiae	[lui:ygl194c] [pn:putative deacetylase:hypothetical 51.5 kd protein in gen1-spo8 intergenic region] [gn:rtl1:g1330] [gtcf:10.1:10.2:10.7] [keggfc:14.2] [sgdfc:4.8:3:6.3:0.9:6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4405	25657050_c1_4	5204	19307	282	94	YGR187C	156	9.5(10)-11	Saccharomyces cerevisiae	[lui:ygr187c] [pn:weak similarity to human hmg1p and hmg2p:hgh1 protein] [gn:hgh1:g7538] [gtcf:10.1] [keggfc:14.2] [sgdfc:9.6:0] [db:gtc-saccharomyces cerevisiae]

CONTIG5063	11765627_f3_7	5205	19308	540	180	YGR187C	326	1.7(10)-29	Saccharomyces cerevisiae	[ui:ygr187c] [pn:weak similarity to human hmg1p and hmg2p:hgh1 protein] [gn:hgh1:g7538] [gtcf:10.1] [keggf:14.2] [sgdfc:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2392	417703_c2_3	5206	19309	291	97	YGR218W	220	6.7(10)-17	Saccharomyces cerevisiae	[ui:ygr218w] [pn:chromosome region maintenance protein:chromosome region maintenance protein 1] [gn:crm1:g8514] [gtcf:10.1] [keggf:14.2] [sgdfc:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2649	21535175_c3_7	5207	19310	1716	572	YGR218W	1870	4.0(10)-193	Saccharomyces cerevisiae	[ui:ygr218w] [pn:chromosome region maintenance protein:chromosome region maintenance protein 1] [gn:crm1:g8514] [gtcf:10.1] [keggf:14.2] [sgdfc:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4726	26594678_c2_5	5208	19311	378	126	YGR218W	344	3.8(10)-30	Saccharomyces cerevisiae	[ui:ygr218w] [pn:chromosome region maintenance protein:chromosome region maintenance protein 1] [gn:crm1:g8514] [gtcf:10.1] [keggf:14.2] [sgdfc:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2558	14554537_c3_4	5209	19312	1476	492	YJL074C	152	3.7(10)-7	Saccharomyces cerevisiae	[ui:yj1074c] [pn:required for structural maintenance of chromosomes:hypothetical 141.3 kd protein in scp160-mrp18 intergenic region] [gn:smc3:j1049] [gtcf:10.1:12.8] [keggf:14.2] [sgdfc:3.8.0:9.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5286	13953792_fl_1	5210	19313	3522	1174	YJL074C	1049	5.5(10)-171	Saccharomyces cerevisiae	[ui:yj074c] [pn:required for structural maintenance of chromosomes:hypothetical 141.3 kd protein in scp160-mpl8 intergenic region] [gn:smc3:j1049] [gtcf:10.1:12.8] [keggf:14.2] [sgdfc:3.8.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5470	22383430_c1_8	5211	19314	603	201	YKR048C	289	1.3(10)-25	Saccharomyces cerevisiae	[ui:ykr048c] [pn:nucleosome assembly protein i:nucleosome assembly protein] [gn:nap1] [gtcf:10.1:12.16:12.8] [keggf:14.2] [sgdfc:3.8.0:6.4.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5416	21502177_c3_15	5212	19315	1080	360	YLR321C	314	3.2(10)-28	Saccharomyces cerevisiae	[ui:yrl321c] [pn:subunit of the rsc complex] [gn:sfh1] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.8.0:4.8.2.4.8.3:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5399	9851537_c1_11	5213	19316	1446	482	YML102W	578	3.3(10)-56	Saccharomyces cerevisiae	[ui:yml102w] [pn:chromatin assembly complex, subunit p60] [gn:cac2] [gtcf:10.1:10.2:10.8:12.16] [keggf:14.2] [sgdfc:3.6.0:4.8.3.6.4.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5164	15117178_c1_6	5214	19317	291	97	YOR213C	180	5.0(10)-14	Saccharomyces cerevisiae	[ui:yor213c] [pn:subunit of the rsc complex] [gtcf:10.1:10.2:12.8] [keggf:14.2] [sgdfc:3.8.0:4.8.2.4.8.3:9.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5335	10553175_c1_7	5215	19318	597	199	YPL254W	94	0.00069	Saccharomyces cerevisiae	[ui:ypl254w] [pn:interacts functionally with histone h2a] [gn:hfl1] [gtcf:10.1] [keggfc:14.2] [sgdfc:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4964	5901551_fl_3	5216	19319	447	149	YPL127C	144	6.0(10)-10	Saccharomyces cerevisiae	[ui:ypl127c] [pn:histone h1 protein:histone h1-like protein] [gn:hho1:lpil7c] [gtcf:10.1:12.8] [keggfc:13.3] [sgdfc:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1370	16596905_c3_1	5217	19320	504	168	YPR018W	101	0.0051	Saccharomyces cerevisiae	[ui:ypr018w] [pn:chromatin assembly complex, subunit p90] [gn:rif2] [gtcf:10.1:10.2:10.8:12.16] [keggfc:14.2] [sgdfc:3.6.0:4.8.3:6.4.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3073	239062_c2_4	5218	19321	1266	422	YPR018W	188	2.8(10)-12	Saccharomyces cerevisiae	[ui:ypr018w] [pn:chromatin assembly complex, subunit p90] [gn:rif2] [gtcf:10.1:10.2:10.8:12.16] [keggfc:14.2] [sgdfc:3.6.0:4.8.3:6.4.0:9.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2829	23601500_c2_5	5219	19322	702	234	YDR002W	531	5.5(10)-61	Saccharomyces cerevisiae	[ui:ydr002w] [pn:ran-specific gtpase-activating protein:ran binding protein 1 homolog:ranbp1:perinuclear array-localised protein] [gn:htn1:sfo1:yrb1:cst20:yd8119] [gtcf:10.1:12.3] [keggfc:14.2] [sgdfc:4.11.0.8.1.0:9.2.0] [db:gtc-sacc

CONTIG1914	23524135_c1_6	5220	19323	258	86	YER110C	231	4.7(10)-18	Saccharomyces cerevisiae	[ui:yer110c] [pn:ran-binding protein:hypothetical 122.6 kd region in nup157-swi4 intergenic region] [gn:kap123] [gtcf:10.1:12.3] [keggfc:14.2] [sgdfc:4.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5421	30081437_c1_8	5221	19324	630	210	YER110C	268	5.2(10)-22	Saccharomyces cerevisiae	[ui:yer110c] [pn:ran-binding protein:hypothetical 122.6 kd region in nup157-swi4 intergenic region] [gn:kap123] [gtcf:10.1:12.3] [keggfc:14.2] [sgdfc:4.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5421	26595180_c2_11	5222	19325	2253	751	YER110C	1589	2.5(10)-163	Saccharomyces cerevisiae	[ui:yer110c] [pn:ran-binding protein:hypothetical 122.6 kd region in nup157-swi4 intergenic region] [gn:kap123] [gtcf:10.1:12.3] [keggfc:14.2] [sgdfc:4.11.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3475	23438412_c2_6	5223	19326	615	205	YIR011C	140	3.3(10)-9	Saccharomyces cerevisiae	[ui:yir011c] [pn:required for transport of mal5p from the cytoplasm to the nucleus:dbf8 protein] [gn:dbf8:stl:yib11c] [gtcf:12.3:10.1] [keggfc:14.2] [sgdfc:4.11.0:8.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG384	4492217_c3_4	5224	19327	1062	354	YMR235C	603	7.5(10)-59	Saccharomyces cerevisiae	[ui:ymr235c] [pn:gtase activating protein:ran gtpase activating protein:protein involved in ma production/processing] [gn:mal:ym9959] [gtfc:10.1:10.3:10.6:12.3] [keggfc:14.2] [sgdfc:4.2:0.4:5.0:4.1:1.0:9.2:0] [db:gtc-saccharomyce]
CONTIG3429	24317187_c2_4	5225	19328	2217	739	YOR160W	1317	1.6(10)-134	Saccharomyces cerevisiae	[ui:yor160w] [pn:involved in mma transport] [gn:mr10] [gtfc:12.3:10.1] [keggfc:14.2] [sgdfc:4.1:1.0:8.1:0] [db:gtc-saccharomyces cerevisiae]
CONTIG4250	11115780_f2_2	5226	19329	564	188	YAL005C	329	4.7(10)-29	Saccharomyces cerevisiae	[ui:yal005c] [pn:heat shock protein of hsp70 family, cytosolic:heat shock protein:heat shock protein yg100] [gn:ssa1] [gtfc:12.7:10.7:13.2] [keggfc:14.2] [sgdfc:6.1:0:6.2:0:8.1:0:9.1:0:9.2:0:1.1:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5363	5110625_c2_24	5227	19330	1101	367	YBR017C	431	1.3(10)-39	Saccharomyces cerevisiae	[ui:ybr017c] [pn:karyopherin:hypothetical 103.7 kd protein in ttp1-gal7 intergenic region] [gn:kap104:ybr017w:ybr0224] [gtfc:10.1] [keggfc:14.2] [sgdfc:8.1:0:9.2:0] [db:gtc-saccharomyces cerevisiae]

CONTIG5363	5281253_c1_18	5228	19331	1668	556	YBR017C	423	3.1(10)-66	Saccharomyces cerevisiae	[ui:ybr017c] [pn:karyopherin:hypothetical 103.7 kd protein in ttp1-gal7 intergenic region] [gn:kap104:ybr017w:ybr0224] [gtcf:10.1] [keggf:14.2] [sgdf:8.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1592	30506930_c1_1	5229	19332	741	247	YBR170C	786	3.1(10)-78	Saccharomyces cerevisiae	[ui:ybr170c] [pn:nuclear protein localization factor and er translocation component:npl4 protein] [gn:npl4:ybr1231] [gtcf:10.1:10.7:11.1:12.16] [keggf:14.2] [sgdf:6.2.0:8.1.0:8.8.0] [db:gtc-saccharomyces cerevisiae]
b3x18484.y	15642686_c2_1	5230	19333	387	129	YER009W	542	2.2(10)-52	Saccharomyces cerevisiae	[ui:yer009w] [pn:nuclear transport factor:nuclear transport factor 2:ntf-2:nuclear transport factor p10] [gn:ntf2] [gtcf:10.1:12.6] [keggf:14.2] [sgdf:8.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3257	3022780_f1_1	5231	19334	1128	376	YIL063C	190	3.5(10)-13	Saccharomyces cerevisiae	[ui:yil063c] [pn:similarity to s.pombe brefeldin a resistance protein and yrb1p:hypothetical 36.1 kd protein in mr3-snp1 intergenic region] [gn:yrb2] [gtcf:10.1:11.1] [keggf:14.2] [sgdf:8.1.0:9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2639	25410253_c3_7	5232	19335	243	81	YLR347C	215	1.7(10)-16	Saccharomyces cerevisiae	[ui:yli347c] [pn:karyopherin-beta] [gn:kap95] [gtcf:10.1:10.7:11.1] [keggfc:14.2] [sgdfc:6.2:0.8:1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2639	7160212_c3_6	5233	19336	261	87	YLR347C	202	4.0(10)-15	Saccharomyces cerevisiae	[ui:yli347c] [pn:karyopherin-beta] [gn:kap95] [gtcf:10.1:10.7:11.1] [keggfc:14.2] [sgdfc:6.2:0.8:1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5020	37500_c2_10	5234	19337	1239	413	YLR347C	1012	3.3(10)-102	Saccharomyces cerevisiae	[ui:yli347c] [pn:karyopherin-beta] [gn:kap95] [gtcf:10.1:10.7:11.1] [keggfc:14.2] [sgdfc:6.2:0.8:1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3033	4179755_fl_1	5235	19338	1314	438	YPL174C	188	9.6(10)-16	Saccharomyces cerevisiae	[ui:ypl174c] [pn:nuclear import protein:protein] [gn:nip80] [gtcf:10.1] [keggfc:14.2] [sgdfc:8.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5689	23484437_fl_2	5236	19339	2472	824	YBR073W	1073	2.6(10)-121	Saccharomyces cerevisiae	[ui:ybr073w] [pn:required for meiosis:hypothetical 108.0 kd helicase in hsp26-sec18 intergenic region] [gn:rdh54:ybr0715] [gtcf:10.10:10.8:12.8] [keggfc:14.2] [sgdfc:3.5:0.3:7.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3226	13759687_b3_5	5237	19340	1782	594	YDL088C	184	3.2(10)-18	Saccharomyces cerevisiae	[ui:ydl088c] [pn:suppressor of temperature-sensitive mutations in pol3p] [gn:asm4] [gtcf:10.10] [keggfc:14.2] [sgdfc:11.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG2898	10719562_f2_1	5238	19341	576	192	YDR061W	285	1.7(10)-24	Saccharomyces cerevisiae	[ui:ydr061w] [pn:similarity to e.coli modf and photorepair protein phra] [gtcf:10.10] [keggfc:14.2] [sgdfc:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3624	4773567_f3_2	5239	19342	918	306	YDR061W	309	3.8(10)-27	Saccharomyces cerevisiae	[ui:ydr061w] [pn:similarity to e.coli modf and photorepair protein phra] [gtcf:10.10] [keggfc:14.2] [sgdfc:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1861	24804700_c2_4	5240	19343	633	211	YDR460W	123	2.5(10)-7	Saccharomyces cerevisiae	[ui:ydr460w] [pn:tfiih subunit:transcription/repair factor] [gn:tfb3] [gtcf:10.10:10.2:12.16] [keggfc:14.2] [sgdfc:4.8.1:6.4.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1861	22275312_c1_3	5241	19344	387	129	YDR460W	391	2.2(10)-36	Saccharomyces cerevisiae	[ui:ydr460w] [pn:tfiih subunit:transcription/repair factor] [gn:tfb3] [gtcf:10.10:10.2:12.16] [keggfc:14.2] [sgdfc:4.8.1:6.4.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5225	22464786_f2_3	5242	19345	852	284	YEL019C	169	1.6(10)-12	Saccharomyces cerevisiae	[ui:yel019c] [pn:dna repair protein] [gn:mms21] [gtcf:10.10:10.8] [keggfc:14.2] [sgdfc:3.7.0:11.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG580	179661_f1_2	5243	19346	618	206	YER176W	350	9.4(10)-31	Saccharomyces cerevisiae	[ui:yer176w] [pn:dna dependent atpase/dna helicase b:hypothetical 127.0 kd protein in rad24-bmh1 intergenic region] [gn:sygp-orf61] [gtcf:10.10:10.8] [keggf:14.2] [sgdfc:3.6.0:3.7.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG580	34102067_f1_3	5244	19347	2754	918	YER176W	1340	6.0(10)-137	Saccharomyces cerevisiae	[ui:yer176w] [pn:dna dependent atpase/dna helicase b:hypothetical 127.0 kd protein in rad24-bmh1 intergenic region] [gn:sygp-orf61] [gtcf:10.10:10.8] [keggf:14.2] [sgdfc:3.6.0:3.7.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG55	10198760_f3_1	5245	19348	609	203	YFR038W	589	2.2(10)-57	Saccharomyces cerevisiae	[ui:yfr038w] [pn:strong similarity to mouse lymphocyte specific helicase:hypothetical 88.7 kd helicase in cdc26-sap155 intergenic region] [gtcf:10.10] [keggf:14.2] [sgdfc:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG440	22273389_c1_2	5246	19349	1224	408	YFR038W	465	1.3(10)-43	Saccharomyces cerevisiae	[ui:yfr038w] [pn:strong similarity to mouse lymphocyte specific helicase:hypothetical 88.7 kd helicase in cdc26-sap155 intergenic region] [gtcf:10.10] [keggf:14.2] [sgdfc:11.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG3831	25443877_c3_3	5247	19350	2007	669	YIL128W	498	6.0(10)-53	Saccharomyces cerevisiae	[ui:yil128w] [pn:involved in ner repair and ma polymerase ii transcription:hypothetical 117.9 kd protein in flk1-sth1 intergenic region] [gn:met18] [gtcf:10.10:10.2] [keggf:14.2] [sgdf:4.8.1:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5589	26439630_c2_16	5248	19351	1602	534	YLR005W	651	1.1(10)-103	Saccharomyces cerevisiae	[ui:ylr005w] [pn:tfiih subunit:transcription initiation factor, factor b:suppressor of stem-loop protein 1] [gn:ssl1] [gtcf:10.10:10.2:10.7] [keggf:14.2] [sgdf:4.8.1:5.2.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1262	9848453_c1_6	5249	19352	696	232	YLR288C	124	7.5(10)-9	Saccharomyces cerevisiae	[ui:ylr288c] [pn:g2-specific checkpoint protein] [gn:mec3] [gtcf:10.10:10.8:12.8] [keggf:14.2] [sgdf:3.7.0:3.8.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1590	24409805_f2_3	5250	19353	915	305	YOL043C	486	1.8(10)-46	Saccharomyces cerevisiae	[ui:yol043c] [pn:endonuclease iii-like glycosylase 2] [gn:ng2] [gtcf:10.10] [keggf:14.2] [sgdf:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2962	14641943_c2_4	5251	19354	852	284	YOR206W	809	1.1(10)-80	Saccharomyces cerevisiae	[ui:yor206w] [pn:strong similarity to rad4p:hypothetical 84.4 kd protein in rpc2/ret1 3''region] [gn:yox001] [gtcf:10.10] [keggf:14.2] [sgdf:11.2.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5003	13750026_f2_5	5252	19355	915	305	YOR206W	368	3.7(10)-33	Saccharomyces cerevisiae	[ui:yor206w] [pn:strong similarity to rad4p:hypothetical 84.4 kd protein in rpc2/ret1 3"region] [gn:yox001] [gtcf:10.10] [keggf:14.2] [sgdfc:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5003	12140763_f3_6	5253	19356	567	189	YOR206W	493	4.2(10)-47	Saccharomyces cerevisiae	[ui:yor206w] [pn:strong similarity to rad4p:hypothetical 84.4 kd protein in rpc2/ret1 3"region] [gn:yox001] [gtcf:10.10] [keggf:14.2] [sgdfc:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5606	6054715_c3_50	5254	19357	1146	382	YOR368W	301	7.5(10)-27	Saccharomyces cerevisiae	[ui:yor368w] [pn:dna damage checkpoint control protein] [gn:rad17] [gtcf:10.10:12.8] [keggf:14.2] [sgdfc:3.5.0:3.8.0:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5807	860175_c3_23	5255	19358	1524	508	YPL122C	683	2.7(10)-123	Saccharomyces cerevisiae	[ui:ypl122c] [pn:tfiih subunit:transcription/repair factor] [gn:tfb2] [gtcf:10.10:10.2] [keggf:14.2] [sgdfc:4.8.1:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4935	24610337_f3_3	5256	19359	1128	376	YPR056W	453	1.8(10)-64	Saccharomyces cerevisiae	[ui:yp056w] [pn:component of rna polymerase transcription initiation tfiih factor] [gtcf:10.10:10.2] [keggf:14.2] [sgdfc:4.8.1:11.2.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5522	36360905_f1_3	5257	19360	789	263	YGL213C	243	2.1(10)-20	Saccharomyces cerevisiae	[ui:ygl213c] [pn:antiviral protein of the beta-transducin:wd-40 repeat family:antiviral protein] [gn:ski8] [gtcf:10.10:12.14] [keggf:14.2] [sgdfc:11.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5522	4897306_f2_7	5258	19361	495	165	YGL213C	358	6.9(10)-33	Saccharomyces cerevisiae	[ui:ygl213c] [pn:antiviral protein of the beta-transducin-wd-40 repeat family:antiviral protein] [gn:ski8] [gtcf:10.10.12.14] [keggf:14.2] [sgdf:11.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1373	11909444_c2_2	5259	19362	666	222	YBL041W	916	5.0(10)-92	Saccharomyces cerevisiae	[ui:ybl041w] [pn:multicatalytic endopeptidase complex subunit:potential proteasome component c5:multicatalytic endopeptidase complex subunit c5] [gn:prs3;pre7;pts1;ybl0407] [gtcf:10.11:14.1] [ec:3.4.99.46] [keggf:14.1] [sgdf:6.5.1;
CONTIG1643	30350813_f2_1	5260	19363	597	199	YBR058C	382	1.7(10)-34	Saccharomyces cerevisiae	[ui:ybr058c] [pn:ubiquitin specific protease:ubiquitin carboxyl-terminal hydrolase 14:ubiquitin thiolesterase 14:ubiquitin-specific processing protease 14:deubiquitinating enzyme 14] [gn:ubp14;ybr0515] [gtcf:10.11] [ec:3.1.2.15] [keg
CONTIG2277	24492311_c2_4	5261	19364	678	226	YBR058C	271	1.5(10)-22	Saccharomyces cerevisiae	[ui:ybr058c] [pn:ubiquitin specific protease:ubiquitin carboxyl-terminal hydrolase 14:ubiquitin thiolesterase 14:ubiquitin-specific processing protease 14:deubiquitinating enzyme 14] [gn:ubp14;ybr0515] [gtcf:10.11] [ec:3.1.2.15] [keg

b2x12892.y	13835917_c1_2	5262	19365	438	146	YBR082C	699	5.0(10)-69	Saccharomyces cerevisiae	[ui:ybr082c] [pn:ubiquitin-conjugating enzyme e2-16 kd:ubiquitin-protein ligase:ubiquitin carrier protein] [gn:ubc4:ybr0745] [gtcfc:10.11:12.9:13.2:14.1] [ec:6.3.2.19] [keggfc:14.1] [sgdgc:3.3.0:6.5.1:9.2]
CONTIG5492	24412517_c3_15	5263	19366	3246	1082	YDL190C	1724	1.2(10)-177	Saccharomyces cerevisiae	[ui:ydl190c] [pn:ubiquitin fusion degradation protein:ub fusion degradation protein 2] [gn:ufd2:d1255] [gtcfc:10.11] [keggfc:14.2] [sgdgc:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1035	10634680_c3_2	5264	19367	720	240	YDL132W	612	8.4(10)-60	Saccharomyces cerevisiae	[ui:ydl132w] [pn:controls gl/s transition] [gn:cdc53] [gtcfc:10.11:12.8] [keggfc:13.3] [sgdgc:3.8.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2950	992030_c3_5	5265	19368	1866	622	YDL132W	140	1.0(10)-14	Saccharomyces cerevisiae	[ui:ydl132w] [pn:controls gl/s transition] [gn:cdc53] [gtcfc:10.11:12.8] [keggfc:13.3] [sgdgc:3.8.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
b9x12j03.y	271937_c1_1	5266	19369	630	210	YDL132W	199	8.0(10)-15	Saccharomyces cerevisiae	[ui:ydl132w] [pn:controls gl/s transition] [gn:cdc53] [gtcfc:10.11:12.8] [keggfc:13.3] [sgdgc:3.8.0:6.5.1] [db:gtc-saccharomyces cerevisiae]

CONTIG1905	12601703_f3_4	5267	19370	342	114	YDL126C	290	1.5(10)-24	Saccharomyces cerevisiae	[ui:ydl126c] [pn:mitochondrial protein of /pas1/sec18 family of atpases:cell division control protein 48] [gn:cdc48] [gtcf:10.11:12.8] [keggf:14.2] [sgdfc:3.8.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5516	6500_f3_6	5268	19371	2529	843	YDL126C	3106	0	Saccharomyces cerevisiae	[ui:ydl126c] [pn:mitochondrial protein of /pas1/sec18 family of atpases:cell division control protein 48] [gn:cdc48] [gtcf:10.11:12.8] [keggf:14.2] [sgdfc:3.8.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5084	4095180_c2_11	5269	19372	918	306	YDL122W	240	6.0(10)-22	Saccharomyces cerevisiae	[ui:ydl122w] [pn:ubiquitin-specific protease:ubiquitin carboxyl-terminal hydrolase 1:ubiquitin thiolesterase 1:ubiquitin-specific processing protease 1:deubiquitinating enzyme 1] [gn:ubp1] [gtcf:10.11] [ec:3.1.2.15] [keggf:14.1] [sg
CONTIG5129	5081556_f2_4	5270	19373	696	232	YDL122W	157	2.5(10)-10	Saccharomyces cerevisiae	[ui:ydl122w] [pn:ubiquitin-specific protease:ubiquitin carboxyl-terminal hydrolase 1:ubiquitin thiolesterase 1:ubiquitin-specific processing protease 1:deubiquitinating enzyme 1] [gn:ubp1] [gtcf:10.11] [ec:3.1.2.15] [keggf:14.1] [sg

CONTIG5129	13859438_f2_5	5271	19374	588	196	YDL122W	227	7.9(10)-18	Saccharomyces cerevisiae	[ui:ydl122w] [pn:ubiquitin-specific protease:ubiquitin carboxyl-terminal hydrolase 1:ubiquitin thiolesterase 1:ubiquitin-specific processing protease 1:deubiquitinating enzyme 1] [gn:ubp1] [gtcf:10.11] [ec:3.1.2.15] [keggfc:14.1] [sg
CONTIG5760	26602260_f1_3	5272	19375	666	222	YDL064W	596	4.2(10)-58	Saccharomyces cerevisiae	[ui:ydl064w] [pn:ubiquitin-conjugating enzyme:ubiquitin-conjugating enzyme e2-18 kd:ubiquitin-protein ligase:ubiquitin carrier protein] [gn:ubc9] [gtcf:10.11:10.7:12.8] [ec:6.3.2.19] [keggfc:14.1] [sgdfc:3.8.0:6.3.0:6.5.1] [db:gtc-sa
CONTIG4273	26850002_c2_9	5273	19376	702	234	YDL007W	849	6.4(10)-85	Saccharomyces cerevisiae	[ui:ydl007w] [pn:probable component of 26s proteasome complex:26s protease regulatory subunit 4 homolog:tat-binding homolog 5] [gn:yta5:yhs4:d2920] [gtcf:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5610	14644806_c2_15	5274	19377	873	291	YDL007W	681	4.0(10)-67	Saccharomyces cerevisiae	[ui:ydl007w] [pn:probable component of 26s proteasome complex:26s protease regulatory subunit 4 homolog:tat-binding homolog 5] [gn:yta5:yhs4:d2920] [gtcf:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]

CONTIG3149	29464092_c3_3	5275	19378	1614	538	YDR069C	681	4.0(10)-67	Saccharomyces cerevisiae	[ui:ydr069c] [pn:ubiquitin-specific protease:ubiquitin carboxyl-terminal hydrolase 4:ubiquitin thiolesterase 4:ubiquitin-specific processing protease 4:deubiquitinating enzyme 4:vacuole biogenesis protein ssv7] [gn:ubp4:doa4:ssv7:ydr960]
CONTIG5815	14552002_f3_21	5276	19379	567	189	YDR092W	104	1.1(10)-12	Saccharomyces cerevisiae	[ui:ydr092w] [pn:ubiquitin-conjugating enzyme:ubiquitin-conjugating enzyme e2-17.5 kd:ubiquitin-protein ligase:ubiquitin carrier protein] [gn:ubc13:ydr6652] [gtcf:10.11:10.7] [ec:6.3.2.19] [keggfc:14.1] [sgdfc:6.3.0:6.5.1] [db:gtc-sac]
CONTIG894	24414010_c1_2	5277	19380	264	88	YDR177W	237	4.5(10)-20	Saccharomyces cerevisiae	[ui:ydr177w] [pn:ubiquitin-conjugating enzyme:ubiquitin-conjugating enzyme e2-24 kd:ubiquitin- protein ligase:ubiquitin carrier protein] [gn:ubc1:ydr9395] [gtcf:10.11:10.7:12.15:14.1] [ec:6.3.2.19] [keggfc:14.1] [sgdfc:3.4.0:6.3.0:6.5]

CONTIG965	22454057_fl_2	5278	19381	207	69	YDR177W	162	4.0(10)-12	Saccharomyces cerevisiae	[ui:ydr177w] [pn:ubiquitin conjugating enzyme:ubiquitin-conjugating enzyme e2-24 kd:ubiquitin- protein ligase:ubiquitin carrier protein] [gn:ubc1:yd9395] [gtcf:10.11:10.7:12.15:14.1] [ec:6.3.2.19] [keggfc:14.1] [sgdfc:3.4.0:6.3.0:6.5]
CONTIG2882	26384713_c2_4	5279	19382	1119	373	YDR394W	1368	6.5(10)-140	Saccharomyces cerevisiae	[ui:ydr394w] [pn:26s proteasome subunit:26s protease regulatory subunit 6 homolog:ynt1 protein:tat-binding homolog 2] [gn:yta2:ynt1:d9509] [gtcf:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5523	3922777_c1_17	5280	19383	621	207	YER012W	738	3.7(10)-73	Saccharomyces cerevisiae	[ui:yer012w] [pn:26s proteasome subunit c11:proteasome component c11:macropain subunit c11:proteinase ysce subunit 11:multicatalytic endopeptidase complex subunit c11] [gn:pre1] [gtcf:10.11] [ec:3.4.99.46] [keggfc:14.1] [sgdfc:6.5.1:]
CONTIG5728	11218942_f2_7	5281	19384	1290	430	YER021W	779	1.7(10)-77	Saccharomyces cerevisiae	[ui:yer021w] [pn:26s proteasome subunit:proteasome component] [gn:sun2] [gtcf:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]

CONTIG4785	10972161_fl_1	5282	19385	627	209	YER094C	815	2.6(10)-81	Saccharomyces cerevisiae	[ui:yer094c] [pn:26s proteasome subunit:proteasome component:macropain subunit:multicatalytic endopeptidase complex subunit pup3] [gn:pup3] [gtcfc:10.11] [ec:3.4.99.46] [keggfc:14.1] [sgdgc:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2102	22457535_c2_5	5283	19386	942	314	YER098W	165	9.8(10)-20	Saccharomyces cerevisiae	[ui:yer098w] [pn:ubiquitin carboxyl-terminal hydrolase:ubiquitin carboxyl-terminal hydrolase 9:ubiquitin thiolesterase 9:ubiquitin-specific processing protease 9:deubiquitinating enzyme 9] [gn:ubp9] [gtcfc:10.11] [ec:3.1.2.15] [keggfc]
b2x17720.x	22470307_c3_5	5284	19387	735	245	YER098W	221	3.1(10)-17	Saccharomyces cerevisiae	[ui:yer098w] [pn:ubiquitin carboxyl-terminal hydrolase:ubiquitin carboxyl-terminal hydrolase 9:ubiquitin thiolesterase 9:ubiquitin-specific processing protease 9:deubiquitinating enzyme 9] [gn:ubp9] [gtcfc:10.11] [ec:3.1.2.15] [keggfc]

CONTIG4175	10584432_f3_3	5285	19388	777	259	YER100W	609	1.7(10)-59	Saccharomyces cerevisiae	[ui:yer100w] [pn:ubiquitin-conjugating enzyme e2-28.4 kd:ubiquitin- protein ligase:ubiquitin carrier protein] [gn:ubc6:doa2] [gtcf:10.11:10.7:12.16:12.9] [ec:6.3.2.19] [keggfc:14.1] [sgdfc:3.3.0:6.3.0:6.5]
CONTIG1561	12773437_c3_7	5286	19389	1044	348	YER151C	140	2.8(10)-10	Saccharomyces cerevisiae	[ui:yer151c] [pn:ubiquitin-specific proteinase:ubiquitin carboxyl-terminal hydrolase 3:ubiquitin thiolesterase 3:ubiquitin-specific processing protease 3:deubiquitinating enzyme 3] [gn:ubp3] [gtcf:10.11] [ec:3.1.2.15] [keggfc:14.1] [
b9x11r65.x	3010967_f2_1	5287	19390	276	92	YER151C	217	1.1(10)-16	Saccharomyces cerevisiae	[ui:yer151c] [pn:ubiquitin-specific proteinase:ubiquitin carboxyl-terminal hydrolase 3:ubiquitin thiolesterase 3:ubiquitin-specific processing protease 3:deubiquitinating enzyme 3] [gn:ubp3] [gtcf:10.11] [ec:3.1.2.15] [keggfc:14.1] [
CONTIG2463	34272812_f1_1	5288	19391	864	288	YFR050C	752	1.2(10)-74	Saccharomyces cerevisiae	[ui:yfr050c] [pn:26s proteasome subunit:proteasome component:macropain subunit:proteinase ysce subunit pre4:multicatalytic endopeptidase complex subunit pre4] [gn:pre4] [gtcf:10.11] [ec:3.4.99.46] [keggfc:14.1] [sgdfc:6.5.1:9.2.0] [d

CONTIG4163	24398262_f2_2	5289	19392	888	296	YFR052W	403	1.2(10)-37	Saccharomyces cerevisiae	[ui:yfr052w] [pn:26s proteasome regulatory subunit:nuclear integrity protein 1] [gn:nin1] [gtcf:10.11:12.8:13.2] [keggfc:14.2] [sgdfc:3.8.0:6.5.1:9.2.0:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2706	19532125_c2_4	5290	19393	450	150	YGL087C	428	2.6(10)-40	Saccharomyces cerevisiae	[ui:ygl087c] [pn:similarity to ubiquitin--protein ligase:hypothetical 15.5 kd protein in mfa12-mad1 intergenic region] [gtcf:10.11:10.7] [keggfc:14.2] [sgdfc:6.3.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1103	12282626_f2_3	5291	19394	417	139	YGL048C	335	1.8(10)-30	Saccharomyces cerevisiae	[ui:ygl048c] [pn:26s proteasome subunit:26s protease regulatory subunit 8 homolog:sug1 protein:cim3 protein:tat-binding protein tby1] [gn:sug1:tby1:tby:cim3:crl3] [gtcf:10.11:12.8] [keggfc:14.2] [sgdfc:3.8.0:6.5.1] [db:gtc-saccharom]
CONTIG2002	12282626_f3_3	5292	19395	957	319	YGL048C	1184	2.0(10)-120	Saccharomyces cerevisiae	[ui:ygl048c] [pn:26s proteasome subunit:26s protease regulatory subunit 8 homolog:sug1 protein:cim3 protein:tat-binding protein tby1] [gn:sug1:tby1:tby:cim3:crl3] [gtcf:10.11:12.8] [keggfc:14.2] [sgdfc:3.8.0:6.5.1] [db:gtc-saccharom]

CONTIG783	4116567_f2_1	5293	19396	249	83	YGL048C	355	1.3(10)-32	Saccharomyces cerevisiae	[ui:ygl048c] [pn:26s proteasome subunit:26s protease regulatory protein:cm3 protein:tat-binding protein tby1] [gn:sug1:tby1:tbyy:cm3:cri3] [gtcf:10.11:12.8] [keggf:14.2] [sgdfc:3.8.0:6.5.1] [db:gtc-saccharom]
CONTIG4529	20009682_c2_9	5294	19397	732	244	YGL011C	784	5.0(10)-78	Saccharomyces cerevisiae	[ui:ygl011c] [pn:26s proteasome subunit yc7alpha/y8:proteasome component c7-alpha:macropain subunit c7-alpha:proteinase ysce subunit 7:multicatalytic endopeptidase complex c7:component y8:sc11 suppressor protein] [gn:prs2:prc2:sc11] [g
CONTIG4962	789628_f2_4	5295	19398	1059	353	YGR048W	771	1.2(10)-76	Saccharomyces cerevisiae	[ui:ygr048w] [pn:ubiquitin fusion degradation protein:ub fusion degradation protein 1] [gn:ufd1] [gtcf:10.11] [keggf:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5108	5960292_f1_1	5296	19399	234	78	YGR048W	151	2.7(10)-10	Saccharomyces cerevisiae	[ui:ygr048w] [pn:ubiquitin fusion degradation protein:ub fusion degradation protein 1] [gn:ufd1] [gtcf:10.11] [keggf:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5107	20414682_c2_9	5297	19400	771	257	YGR135W	788	1.8(10)-78	Saccharomyces cerevisiae	[ui:ygr135w] [pn:26s proteasome subunit y13:proteasome component y13:macropain subunit y13:proteinase ysce subunit 13:multicatalytic endopeptidase complex subunit y13] [gn:prs5:pre9] [gtcf:10.11] [ec:3.4.99.46] [keggfc:14.1] [sgdfc:6]
CONTIG1129	25572906_c2_2	5298	19401	1305	435	YGR184C	178	6.0(10)-10	Saccharomyces cerevisiae	[ui:ygr184c] [pn:ubiquitin-protein ligase:n-end-recognizing protein:ubiquitin-protein ligase e3 component:n-recognin] [gn:ubrl:g7168] [gtcf:10.11] [keggfc:14.2] [sgdfc:6.5.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4544	32619157_f2_1	5299	19402	2454	818	YGR184C	165	4.7(10)-13	Saccharomyces cerevisiae	[ui:ygr184c] [pn:ubiquitin-protein ligase:n-end-recognizing protein:ubiquitin-protein ligase e3 component:n-recognin] [gn:ubrl:g7168] [gtcf:10.11] [keggfc:14.2] [sgdfc:6.5.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4837	594792_f3_2	5300	19403	1896	632	YGR184C	728	1.2(10)-70	Saccharomyces cerevisiae	[ui:ygr184c] [pn:ubiquitin-protein ligase:n-end-recognizing protein:ubiquitin-protein ligase e3 component:n-recognin] [gn:ubrl:g7168] [gtcf:10.11] [keggfc:14.2] [sgdfc:6.5.1:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4837	12503175_fl_1	5301	19404	1488	496	YGR184C	104	0.096	Saccharomyces cerevisiae	[ui: ygr184c] [pn: ubiquitin-protein ligase: n-end-recognizing protein: ubiquitin-protein ligase e3 component: n-recognin] [gn: ubr1: g7168] [gtcf: 10.11] [keggf: 14.2] [sgdf: 6.5.1: 9.2.0] [db: gtc-saccharomyces cerevisiae]
CONTIG3090	26298260_c1_2	5302	19405	303	101	YGR253C	267	3.0(10)-23	Saccharomyces cerevisiae	[ui: ygr253c] [pn: 26s proteasome subunit: proteasome component pup2: macropain subunit pup2: proteinase ysce subunit pup2: multicatalytic endopeptidase complex subunit pup2] [gn: pup2: doa5] [gtcf: 10.11: 12.8] [ec: 3.4.99.46] [keggf: 14.1] [s
CONTIG355	1204657_c3_5	5303	19406	315	105	YGR253C	395	8.3(10)-37	Saccharomyces cerevisiae	[ui: ygr253c] [pn: 26s proteasome subunit: proteasome component pup2: macropain subunit pup2: proteinase ysce subunit pup2: multicatalytic endopeptidase complex subunit pup2] [gn: pup2: doa5] [gtcf: 10.11: 12.8] [ec: 3.4.99.46] [keggf: 14.1] [s
CONTIG5713	4882176_f3_6	5304	19407	1227	409	YGR270W	200	2.0(10)-13	Saccharomyces cerevisiae	[ui: ygr270w] [pn: 26s proteasome subunit: tat-binding homolog 7] [gn: yta7] [gtcf: 10.11] [keggf: 14.2] [sgdf: 6.5.1] [db: gtc-saccharomyces cerevisiae]
CONTIG5713	40677_fl_3	5305	19408	2760	920	YGR270W	1743	3.2(10)-186	Saccharomyces cerevisiae	[ui: ygr270w] [pn: 26s proteasome subunit: tat-binding homolog 7] [gn: yta7] [gtcf: 10.11] [keggf: 14.2] [sgdf: 6.5.1] [db: gtc-saccharomyces cerevisiae]

CONTIG1924	11907192_fl_1	5306	19409	660	220	YHR027C	511	3.7(10)-48	Saccharomyces cerevisiae	[ui:yhr027c] [pn:subunit of the 26s proteasome:hypothetical 109.5 kd protein in ppal-dap2 intergenic region] [gn:hrd2] [gtcf:10.11] [keggf:14.2] [sgdf:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2755	24665942_fl_1	5307	19410	468	156	YHR027C	479	1.1(10)-44	Saccharomyces cerevisiae	[ui:yhr027c] [pn:subunit of the 26s proteasome:hypothetical 109.5 kd protein in ppal-dap2 intergenic region] [gn:hrd2] [gtcf:10.11] [keggf:14.2] [sgdf:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2755	6835138_fl_2	5308	19411	249	83	YHR027C	256	8.5(10)-21	Saccharomyces cerevisiae	[ui:yhr027c] [pn:subunit of the 26s proteasome:hypothetical 109.5 kd protein in ppal-dap2 intergenic region] [gn:hrd2] [gtcf:10.11] [keggf:14.2] [sgdf:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG2755	25581512_fl_3	5309	19412	978	326	YHR027C	430	2.0(10)-39	Saccharomyces cerevisiae	[ui:yhr027c] [pn:subunit of the 26s proteasome:hypothetical 109.5 kd protein in ppal-dap2 intergenic region] [gn:hrd2] [gtcf:10.11] [keggf:14.2] [sgdf:6.5.1] [db:gtc-saccharomyces cerevisiae]
b3x12710.x	24414075_f2_2	5310	19413	213	71	YHR027C	106	8.9(10)-5	Saccharomyces cerevisiae	[ui:yhr027c] [pn:subunit of the 26s proteasome:hypothetical 109.5 kd protein in ppal-dap2 intergenic region] [gn:hrd2] [gtcf:10.11] [keggf:14.2] [sgdf:6.5.1] [db:gtc-saccharomyces cerevisiae]

CONTIG2548	20881662_f3_2	5311	19414	741	247	YHR200W	514	2.0(10)-49	Saccharomyces cerevisiae	[ui:yhr200w] [pn:26s proteasome subunit:26s proteasome regulatory subunit] [gn:sun1] [gtcf:10.11] [keggf:14.2] [sgdf:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5430	34078136_c3_19	5312	19415	2886	962	YIL156W	471	4.7(10)-63	Saccharomyces cerevisiae	[ui:yil156w] [pn:ubiquitin carboxy terminal hydrolase:ubiquitin carboxyl-terminal hydrolase 7:ubiquitin thiolesterase 7:ubiquitin-specific processing protease 7:deubiquitinating enzyme 7] [gn:ubp7] [gtcf:10.11] [ec:3.1.2.15] [keggf:
CONTIG2488	12925375_c3_8	5313	19416	543	181	YIL075C	304	5.7(10)-26	Saccharomyces cerevisiae	[ui:yil075c] [pn:26s proteasome regulatory subunit:tma-processing protein] [gn:sen3] [gtcf:10.11:10.6] [keggf:14.2] [sgdf:4.5.0:6.5.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4919	915882_f3_6	5314	19417	2079	693	YIL075C	1728	4.5(10)-178	Saccharomyces cerevisiae	[ui:yil075c] [pn:26s proteasome regulatory subunit:tma-processing protein] [gn:sen3] [gtcf:10.11:10.6] [keggf:14.2] [sgdf:4.5.0:6.5.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5716	10723752_f2_6	5315	19418	963	321	YJL197W	263	2.2(10)-21	Saccharomyces cerevisiae	[ui:yjl197w] [pn:ubiquitin c-terminal hydrolase:ubiquitin carboxyl-terminal hydrolase 12:ubiquitin thiolesterase 12:ubiquitin-specific processing protease 12:deubiquitinating enzyme 12] [gn:ubp12:j0340] [gtcf:10.11] [ec:3.1.2.15] [ke

CONTIG5716	24728462_fl_2	5316	19419	2142	714	YJL197W	620	6.4(10)-98	Saccharomyces cerevisiae	[ui:yjl197w] [pn:ubiquitin c-terminal hydrolase:ubiquitin carboxyl-terminal hydrolase 12:ubiquitin thiolesterase 12:ubiquitin-specific processing protease 12:deubiquitinating enzyme 12] [gn:ubp12:j0340] [gtcfc:10.11] [ec:3.1.2.15] [ke
CONTIG4322	24647805_fl_1	5317	19420	345	115	YJL001W	299	1.2(10)-26	Saccharomyces cerevisiae	[ui:yjl001w] [pn:multicatalytic endopeptidase complex subunit:proteasome component pre3 precursor:macropain subunit pre3:proteinase ysc subunit pre3:multicatalytic endopeptidase complex subunit pre3] [gn:pre3:j1407] [gtcfc:10.11:12.8]
CONTIG2332	959380_f2_1	5318	19421	810	270	YJR099W	280	1.3(10)-24	Saccharomyces cerevisiae	[ui:yjr099w] [pn:ubiquitin-specific protease:ubiquitin carboxyl-terminal hydrolase yuh1:ubiquitin thiolesterase] [gn:yuh1:j1941] [gtcfc:10.11] [ec:3.1.2.15] [keggfc:14.1] [sgdfc:6.3.0:6.5.1.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1336	3907128_f3_3	5319	19422	867	289	YKL213C	493	4.7(10)-47	Saccharomyces cerevisiae	[ui:ykl213c] [pn:involved in ubiquitin-dependent proteolysis:protein] [gn:doa1] [gtcfc:10.11] [keggfc:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5139	13792203_e2_7	5320	19423	1530	510	YKL213C	512	3.8(10)-58	Saccharomyces cerevisiae	[ui:ykl213c] [pn:involved in ubiquitin-dependent proteolysis:protein] [gn:doa1] [gtcf:10.11] [keggf:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5615	3907128_f1_4	5321	19424	357	119	YKL213C	120	1.8(10)-6	Saccharomyces cerevisiae	[ui:ykl213c] [pn:involved in ubiquitin-dependent proteolysis:protein] [gn:doa1] [gtcf:10.11] [keggf:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1706	1197311_f3_1	5322	19425	1269	423	YKL145W	1401	3.7(10)-176	Saccharomyces cerevisiae	[ui:ykl145w] [pn:26s proteasome subunit:26s protease regulatory subunit 7 homolog:cim5 protein:tat-binding homolog 3] [gn:cim5:yta3] [gtcf:10.11:12.8] [keggf:14.2] [sgdfc:3.8.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1540	25554760_f2_2	5323	19426	1002	334	YKL010C	165	5.5(10)-9	Saccharomyces cerevisiae	[ui:ykl010c] [pn:similarity to rat ubiquitin ligase nedd4:hypothetical 167.8 kd protein cce1-cap1 intergenic region] [gn:ufd4:ykl162] [gtcf:10.11] [keggf:14.2] [sgdfc:6.5.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3231	36531255_f3_3	5324	19427	915	305	YKL010C	397	1.3(10)-35	Saccharomyces cerevisiae	[ui:ykl010c] [pn:similarity to rat ubiquitin ligase nedd4:hypothetical 167.8 kd protein cce1-cap1 intergenic region] [gn:ufd4:ykl162] [gtcf:10.11] [keggf:14.2] [sgdfc:6.5.1:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4051	21734385_c1_4	5325	19428	411	137	YKL010C	449	4.0(10)-41	Saccharomyces cerevisiae	[ui:ykl010c] [pn:similarity to rat ubiquitin ligase nedd4:hypothetical 167.8 kd protein cce1-cap1 intergenic region] [gn:ufd4-ykl162] [gtcf:10.11] [keggf:14.2] [sgdfc:6.5.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4051	19644012_c3_5	5326	19429	1323	441	YKL010C	528	1.5(10)-65	Saccharomyces cerevisiae	[ui:ykl010c] [pn:similarity to rat ubiquitin ligase nedd4:hypothetical 167.8 kd protein cce1-cap1 intergenic region] [gn:ufd4-ykl162] [gtcf:10.11] [keggf:14.2] [sgdfc:6.5.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5676	24397906_fl_1	5327	19430	621	207	YLR167W	545	1.1(10)-52	Saccharomyces cerevisiae	[ui:ylr167w] [pn:ubiquitin/ribosomal protein s27a:ubiquitin] [gn:ubi3:19470] [gtcf:10.11:10.4] [keggf:14.2] [sgdfc:5.1.0:6.5.1:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5781	3990936_c2_24	5328	19431	606	202	YLR306W	417	3.8(10)-39	Saccharomyces cerevisiae	[ui:ylr306w] [pn:ubiquitin-conjugating enzyme e2-21.2 kd:ubiquitin-protein ligase:ubiquitin carrier protein] [gn:ubc12:12142] [gtcf:10.11:10.7] [ec:6.3.2.19] [keggf:14.1] [sgdfc:6.3.0:6.5.1] [db:gtc-sacc]

CONTIG1979	9953462_f2_1	5329	19432	1368	456	YLR452C	285	4.7(10)-52	Saccharomyces cerevisiae	[ui:ymlr452c] [pn:involved in desensitization to alpha-factor pheromone:protein] [gn:ss2] [gtcf:10.11:11.1:12.8:12.9] [keggfc:14.2] [sgdfe:3.3.0:6.5.1:9.1.0:10.1.6] [db:gtc-saccharomyces cerevisiae]
CONTIG5416	32501382_f1_1	5330	19433	1407	469	YML1111W	95	0.34	Saccharomyces cerevisiae	[ui:yml1111w] [pn:strong similarity to ubiquitination protein bull p] [gtcf:10.11:10.7] [keggfc:14.2] [sgdfe:6.3.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5738	986261_c3_21	5331	19434	1158	386	YML1111W	309	1.6(10)-26	Saccharomyces cerevisiae	[ui:yml1111w] [pn:strong similarity to ubiquitination protein bull p] [gtcf:10.11:10.7] [keggfc:14.2] [sgdfe:6.3.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3334	15735437_c1_3	5332	19435	273	91	YML092C	278	2.1(10)-24	Saccharomyces cerevisiae	[ui:yml092c] [pn:26s proteasome subunit y7:proteasome component y7:macropain subunit y7:proteinase ysce subunit 7:multicatalytic endopeptidase complex subunit y7] [gn:prs4:pre8] [gtcf:10.11:12.8] [ec:3.4.99.46] [keggfc:14.1] [sgdfe:6]
CONTIG5642	4771952_f2_4	5333	19436	501	167	YML092C	543	1.7(10)-52	Saccharomyces cerevisiae	[ui:yml092c] [pn:26s proteasome subunit y7:proteasome component y7:macropain subunit y7:proteinase ysce subunit 7:multicatalytic endopeptidase complex subunit y7] [gn:prs4:pre8] [gtcf:10.11:12.8] [ec:3.4.99.46] [keggfc:14.1] [sgdfe:6]

CONTIG5642	22051285_f3_5	5334	19437	534	178	YMR022W	637	1.8(10)-62	Saccharomyces cerevisiae	[ui:ymr022w] [pn:ubiquitin conjugating enzyme:ubiquitin-kd:ubiquitin-protein ligase:ubiquitin carrier protein] [gn:ubc7:qr8:ym9711] [gicf:10.11:10.7:12.16:12.9:13.2] [ec:6.3.2.19] [keggf:14.1] [sgdfc:3.3.0:
CONTIG2798	35367187_f3_3	5335	19438	1212	404	YMR223W	236	3.2(10)-44	Saccharomyces cerevisiae	[ui:ymr223w] [pn:similarity to human putative ubiquitin carboxyl-terminal hydrolase:putative ubiquitin carboxyl-terminal hydrolase ymr223w:ubiquitin thiolesterase:ubiquitin-specific processing protease:deubiquitinating enzyme] [gn:ym99
CONTIG2798	4882180_f3_4	5336	19439	255	85	YMR223W	178	5.5(10)-13	Saccharomyces cerevisiae	[ui:ymr223w] [pn:similarity to human putative ubiquitin carboxyl-terminal hydrolase:putative ubiquitin carboxyl-terminal hydrolase ymr223w:ubiquitin thiolesterase:ubiquitin-specific processing protease:deubiquitinating enzyme] [gn:ym99

CONTIG916	22067010_c1_1	5337	19440	978	326	YMR223W	236	1.0(10)-35	Saccharomyces cerevisiae	[ui:ymr223w] [pn:similarity to human putative ubiquitin carboxyl-terminal hydrolase:putative ubiquitin carboxyl-terminal hydrolase ymr223w:ubiquitin thiolesterase:ubiquitin-specific processing protease:deubiquitinating enzyme] [gn:ym99]
CONTIG18	12312660_f3_1	5338	19441	570	190	YMR275C	95	0.04399	Saccharomyces cerevisiae	[ui:ymr275c] [pn:ubiquitination pathway protein:ubiquitination pathway protein bull:respiration deficiency suppressor] [gn:bull:dag1:rds1:ym8021] [gtcf:10.11:10.7] [keggfc:14.2] [sgdfc:6.3.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1692	35798416_c2_1	5339	19442	1215	405	YMR275C	384	1.7(10)-34	Saccharomyces cerevisiae	[ui:ymr275c] [pn:ubiquitination pathway protein:ubiquitination pathway protein bull:respiration deficiency suppressor] [gn:bull:dag1:rds1:ym8021] [gtcf:10.11:10.7] [keggfc:14.2] [sgdfc:6.3.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4859	2158338_c3_13	5340	19443	1173	391	YMR275C	289	2.5(10)-24	Saccharomyces cerevisiae	[ui:ymr275c] [pn:ubiquitination pathway protein:ubiquitination pathway protein bull:respiration deficiency suppressor] [gn:bull:dag1:rds1:ym8021] [gtcf:10.11:10.7] [keggfc:14.2] [sgdfc:6.3.0:6.5.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5472	24641625_fl_1	5341	19444	1008	336	YMR275C	272	1.6(10)-22	Saccharomyces cerevisiae	[ui:ymr275c] [pn:ubiquitination pathway protein bul1:respiration deficiency suppressor] [gn:bul1:dag1:rdsl:ym8021] [gtcf:10.11:10.7] [keggf:14.2] [sgdf:6.3.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5200	33212758_f3_8	5342	19445	855	285	YMR314W	733	1.3(10)-72	Saccharomyces cerevisiae	[ui:ymr314w] [pn:26s proteasome subunit, alpha-type:proteasome component pre5:macropain subunit pre5:proteinase ysce subunit pre5:multicatalytic endopeptidase complex subunit pre5] [gn:pre5:ym9924] [gtcf:10.11:12.8] [ec:3.4.99.46] [k
CONTIG5810	5083552_fl_5	5343	19446	1614	538	YNL239W	902	1.6(10)-90	Saccharomyces cerevisiae	[ui:ynl239w] [pn:aminopeptidase of cysteine protease family:cysteine proteinase 1:y3:bleomycin hydrolase:blm hydrolase] [gn:blh1:ycp1:lap3:gal6:n118] [gtcf:10.11:5.5] [ec:3.4.22.-] [keggf:14.1] [sgdf:6.5.1:9.2.0] [db:gtc-saccharom
CONTIG4281	20914068_c2_5	5344	19447	735	245	YOL038W	806	2.2(10)-80	Saccharomyces cerevisiae	[ui:yol038w] [pn:multicatalytic endopeptidase complex chain:proteasome component:macropain subunit:proteinase ysce subunit pre6:multicatalytic endopeptidase complex subunit pre6] [gn:pre6] [gtcf:10.11:12.8] [ec:3.4.99.46] [keggf:14.

CONTIG1575	25807938_f1_1	5345	19448	969	323	YOR117W	1160	7.0(10)-118	Saccharomyces cerevisiae	[ui:yor117w] [pn:26s proteasome subunit:probable 26s protease subunit tbp-1:tat-binding protein homolog 1] [gn:ytal:o3258:yor3258w] [gtcf:10.11] [keggf:14.2] [sgdf:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3560	954776_f1_1	5346	19449	1908	636	YOR124C	837	5.5(10)-120	Saccharomyces cerevisiae	[ui:yor124c] [pn:ubiquitin-specific proteinase:ubiquitin carboxyl-terminal hydrolase 2:ubiquitin thiolesterase 2:ubiquitin-specific processing protease 2:deubiquitinating enzyme 2] [gn:ubp2:o3281:yor3281c] [gtcf:10.11] [ec:3.1.2.15]
CONTIG4291	5115900_c3_9	5347	19450	1896	632	YOR124C	190	4.5(10)-19	Saccharomyces cerevisiae	[ui:yor124c] [pn:ubiquitin-specific proteinase:ubiquitin carboxyl-terminal hydrolase 2:ubiquitin thiolesterase 2:ubiquitin-specific processing protease 2:deubiquitinating enzyme 2] [gn:ubp2:o3281:yor3281c] [gtcf:10.11] [ec:3.1.2.15]
CONTIG4662	34656251_f1_2	5348	19451	465	155	YOR157C	504	2.2(10)-48	Saccharomyces cerevisiae	[ui:yor157c] [pn:26s proteasome subunit:proteasome component precursor:macropain subunit:proteinase ysc subunit pup1:multicatalytic endopeptidase complex subunit pup1] [gn:pup1] [gtcf:10.11:12.8] [ec:3.4.99.46] [keggf:14.1] [sgdf:

CONTIG4662	29410912_f2_3	5349	19452	483	161	YOR157C	537	7.4(10)-52	Saccharomyces cerevisiae	[ui:yor157c] [pn:26s proteasome subunit:proteasome component precursor:macropain subunit:protease ysc subunit pup1:multicatalytic endopeptidase complex subunit pup1] [gn:pup1] [gicf:10.11:12.8] [ec:3.4.99.46] [keggf:14.1] [sgdfc:
CONTIG3491	12540827_c2_7	5350	19453	1197	399	YOR259C	1574	9.5(10)-162	Saccharomyces cerevisiae	[ui:yor259c] [pn:26s proteasome subunit:probable 26s protease subunit sug2] [gn:cr13:sug2:cr13_of_yor259c] [gicf:10.11:10.2] [keggf:14.2] [sgdfc:4.8.2:6.5.1] [db:gic-saccharomyces cerevisiae]
CONTIG5559	20423437_f1_4	5351	19454	1029	343	YOR261C	854	1.8(10)-85	Saccharomyces cerevisiae	[ui:yor261c] [pn:strong similarity to human 26s proteasome regulatory chain, p40] [gtcf:10.11] [keggf:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5711	26204426_f1_4	5352	19455	243	81	YOR362C	307	1.7(10)-27	Saccharomyces cerevisiae	[ui:yor362c] [pn:26s proteasome subunit c1:proteasome component c1:macropain subunit c1:proteinase ysc subunit 1:multicatalytic endopeptidase complex subunit c1] [gn:prs1:prc1:pre10] [gicf:10.11:12.8] [ec:3.4.99.46] [keggf:14.1] [s

CONTIG5711	867015_fl_5	5353	19456	516	172	YOR362C	448	2.0(10)-42	Saccharomyces cerevisiae	[ui:yor362c] [pn:26s proteasome subunit c1:proteasome component c1:macropain subunit c1:proteinase ysc subunit 1:multicatalytic endopeptidase complex subunit c1] [gn:prs1:prc1:pre10] [gtcf:10.11:12.8] [ec:3.4.99.46] [keggc:14.1] [s]
CONTIG4364	23626263_c3_8	5354	19457	252	84	YPL074W	244	1.1(10)-19	Saccharomyces cerevisiae	[ui:yp1074w] [pn:similarity to vps4p and yta4p:probable 26s protease subunit:tat-binding homolog 6] [gn:yta6] [gtcf:10.11] [keggc:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4774	40662_fl_2	5355	19458	537	179	YPL074W	440	6.5(10)-41	Saccharomyces cerevisiae	[ui:yp1074w] [pn:similarity to vps4p and yta4p:probable 26s protease subunit:tat-binding homolog 6] [gn:yta6] [gtcf:10.11] [keggc:14.2] [sgdfc:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3898	37900_c1_3	5356	19459	840	280	YPL003W	286	6.5(10)-25	Saccharomyces cerevisiae	[ui:yp1003w] [pn:similarity to ubiquitin-activating enzymes] [gtcf:10.11:10.7] [keggc:14.2] [sgdfc:6.3.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5726	20345018_c2_23	5357	19460	1047	349	YPR066W	564	1.0(10)-54	Saccharomyces cerevisiae	[ui:yp066w] [pn:strong similarity to ubiquitin-activating enzymes] [gtcf:10.11:10.7] [keggc:14.2] [sgdfc:6.3.0:6.5.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5036	21679002_c3_13	5358	19461	942	314	YPR103W	1144	3.5(10)-116	Saccharomyces cerevisiae	[ui:ypr103w] [pn:26s proteasome subunit:proteasome component pre2 precursor:macropain subunit pre2:proteinase ysce subunit pre2:multicatalytic endopeptidase complex subunit pre2] [gn:pre2:prg1:doa3:p8283] [gtcf:10.11:12.8] [ec:3.4.99]
CONTIG2014	23631875_f1_1	5359	19462	912	304	YPR180W	236	5.7(10)-20	Saccharomyces cerevisiae	[ui:ypr180w] [pn:similarity to ubiquitin-activating enzymes] [gtcf:10.11:10.7] [keggf:14.2] [sgdf:6.3.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5485	31672080_f3_5	5360	19463	315	105	YPR180W	181	1.2(10)-13	Saccharomyces cerevisiae	[ui:ypr180w] [pn:similarity to ubiquitin-activating enzymes] [gtcf:10.11:10.7] [keggf:14.2] [sgdf:6.3.0:6.5.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4098	32609638_c2_4	5361	19464	2112	704	YDL077C	283	3.2(10)-21	Saccharomyces cerevisiae	[ui:ydl077c] [pn:vacuolar carboxypeptidase y] [gn:vam6] [gtcf:10.11:12.16] [keggf:14.2] [sgdf:6.5.2:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2363	23627260_c3_5	5362	19465	183	61	YEL060C	144	4.2(10)-9	Saccharomyces cerevisiae	[ui:yel060c] [pn:protease b, vacuolar:cerevisin precursor:vacuolar protease b:proteinase yscb] [gn:prb1] [gtcf:10.11:12.16] [ec:3.4.21.48] [keggf:14.1] [sgdf:6.3.0:6.5.2:9.10.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4372	24429712_fl_3	5363	19466	1068	356	YEL060C	818	1.2(10)-81	Saccharomyces cerevisiae	[ui:yel060c] [pn:protease b, vacuolar:cerevisin precursor:vacuolar protease b:proteinase yscb] [gn:prb1] [gtcf:10.11:12.16] [ec:3.4.21.48] [keggfc:14.1] [sgdfc:6.3.0:6.5.2.9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5557	4105375_c1_15	5364	19467	1041	347	YEL060C	482	5.0(10)-46	Saccharomyces cerevisiae	[ui:yel060c] [pn:protease b, vacuolar:cerevisin precursor:vacuolar protease b:proteinase yscb] [gn:prb1] [gtcf:10.11:12.16] [ec:3.4.21.48] [keggfc:14.1] [sgdfc:6.3.0:6.5.2.9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5557	5256575_c3_19	5365	19468	1209	403	YEL060C	479	1.0(10)-45	Saccharomyces cerevisiae	[ui:yel060c] [pn:protease b, vacuolar:cerevisin precursor:vacuolar protease b:proteinase yscb] [gn:prb1] [gtcf:10.11:12.16] [ec:3.4.21.48] [keggfc:14.1] [sgdfc:6.3.0:6.5.2.9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG809	36047562_f3_2	5366	19469	519	173	YEL060C	501	4.7(10)-48	Saccharomyces cerevisiae	[ui:yel060c] [pn:protease b, vacuolar:cerevisin precursor:vacuolar protease b:proteinase yscb] [gn:prb1] [gtcf:10.11:12.16] [ec:3.4.21.48] [keggfc:14.1] [sgdfc:6.3.0:6.5.2.9.10.0] [db:gtc-saccharomyces cerevisiae]

CONTIG934	9877305_c2_4	5367	19470	243	81	YEL060C	284	3.6(10)-24	Saccharomyces cerevisiae	[ui:yel060c] [pn:protease b, vacuolar:cerevisin precursor:vacuolar protease b;proteinase yscb] [gn:prb1] [gtcf:10.11:12.16] [ec:3.4.21.48] [keggfc:14.1] [sgdfc:6.3.0:6.5.2:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3501	14878552_fl_1	5368	19471	837	279	YHR028C	336	1.6(10)-29	Saccharomyces cerevisiae	[ui:yhr028c] [pn:dipeptidyl aminopeptidase b:dpap b:yscv] [gn:dap2] [gtcf:10.11:12.16] [ec:3.4.14.-] [keggfc:14.1] [sgdfc:6.5.2:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4805	26692808_c2_4	5369	19472	1485	495	YHR028C	1154	3.1(10)-117	Saccharomyces cerevisiae	[ui:yhr028c] [pn:dipeptidyl aminopeptidase b:dpap b:yscv] [gn:dap2] [gtcf:10.11:12.16] [ec:3.4.14.-] [keggfc:14.1] [sgdfc:6.5.2:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3410	9844200_c1_9	5370	19473	876	292	YKL103C	964	4.2(10)-97	Saccharomyces cerevisiae	[ui:ykl103c] [pn:aminopeptidase ysc1 precursor, vacuolar:vacuolar aminopeptidase i precursor:polypeptidase:leucine aminopeptidase:aminopeptidase iii:aminopeptidase ysc1:lapiv] [gn:apel:lap4:ykl455] [gtcf:10.11:12.16] [ec:3.4.11.1] [k

CONTIG3410	36523442_c2_10	5371	19474	876	292	YKL103C	549	4.0(10)-53	Saccharomyces cerevisiae	[ui:ykl103c] [pn:aminopeptidase ysc1 precursor, vacuolar: vacuolar aminopeptidase i precursor: polypeptidase: leucine aminopeptidase: aminopeptidase iii: aminopeptidase ysc1: lapiv] [gn:apel:lap4:ykl455] [gtcf:10.11:12.16] [ec:3.4.11.1] [k
CONTIG4002	36353158_c1_6	5372	19475	954	318	YKL103C	459	1.3(10)-43	Saccharomyces cerevisiae	[ui:ykl103c] [pn:aminopeptidase ysc1 precursor, vacuolar: vacuolar aminopeptidase i precursor: polypeptidase: leucine aminopeptidase: aminopeptidase iii: aminopeptidase ysc1: lapiv] [gn:apel:lap4:ykl455] [gtcf:10.11:12.16] [ec:3.4.11.1] [k
CONTIG4002	11141300_c3_8	5373	19476	852	284	YKL103C	277	1.1(10)-23	Saccharomyces cerevisiae	[ui:ykl103c] [pn:aminopeptidase ysc1 precursor, vacuolar: vacuolar aminopeptidase i precursor: polypeptidase: leucine aminopeptidase: aminopeptidase iii: aminopeptidase ysc1: lapiv] [gn:apel:lap4:ykl455] [gtcf:10.11:12.16] [ec:3.4.11.1] [k
CONTIG5022	24491408_c2_7	5374	19477	1737	579	YMR297W	1588	3.1(10)-163	Saccharomyces cerevisiae	[ui:ymr297w] [pn:carboxypeptidase y, serine-type protease: carboxypeptidase y precursor: carboxypeptidase ysc1] [gn:prc1] [gtcf:10.11:12.16] [keggfc:14.1] [sgdfc:6.5.2:9.10.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5684	4878376_f3_11	5375	19478	1599	533	YMR297W	989	9.4(10)-100	Saccharomyces cerevisiae	[ui:ymr297w] [pn:carboxypeptidase y, serine-type protease:carboxypeptidase y precursor:carboxypeptidase y [gn:prc1] [gtcf:10.11:12.16] [keggf:14.1] [sgdf:6.5.2:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5790	22695252_f1_5	5376	19479	1659	553	YMR297W	1348	8.5(10)-138	Saccharomyces cerevisiae	[ui:ymr297w] [pn:carboxypeptidase y, serine-type protease:carboxypeptidase y precursor:carboxypeptidase y [gn:prc1] [gtcf:10.11:12.16] [keggf:14.1] [sgdf:6.5.2:9.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4471	10970285_c3_11	5377	19480	1008	336	YNR007C	293	5.5(10)-61	Saccharomyces cerevisiae	[ui:ynr007c] [pn:essential for autophagocytosis:hypothetical 35.9 kd protein in vps27-cse2 intergenic region] [gn:aut1:n2040] [gtcf:10.11:12.13] [keggf:14.2] [sgdf:6.5.2:8.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2749	16075_c3_7	5378	19481	1146	382	YPL154C	146	2.2(10)-7	Saccharomyces cerevisiae	[ui:ypl154c] [pn:aspartyl protease:saccharopepsin precursor:aspartate protease:proteinase a:proteinase yscA] [gn:pep4:pho9:pral:p2585] [gtcf:10.11:5.2:7.2] [ec:3.4.23.25] [keggf:14.1] [sgdf:6.3.0:6.5.2:9.10.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5808	24003930_f2_13	5379	19482	1011	337	YPL154C	1342	3.7(10)-137	Saccharomyces cerevisiae	[ui:ypl154c] [pn:aspartyl protease:saccharopepsin precursor:aspartate protease:proteinase a:proteinase yscd] [gn:pep4:pho9:pral:p2585] [gtcfc:10.11:5.2:7.2] [ec:3.4.23.25] [keggfc:14.1] [sgdgc:6.3:0:6.5:2:9.10.0] [db:gtc-saccharomyces]
CONTIG1436	14941251_f1_1	5380	19483	726	242	YCL057W	592	1.1(10)-57	Saccharomyces cerevisiae	[ui:ycl057w] [pn:saccharolysin protease d:proteinase yscd:oligopeptidase yscd] [gn:prd1:ycl57w] [gtcfc:10.11:7.2] [ec:3.4.24.37] [keggfc:14.1] [sgdgc:6.5.3] [db:gtc-saccharomyces cerevisiae]
CONTIG1436	3015887_f2_2	5381	19484	204	68	YCL057W	152	7.0(10)-10	Saccharomyces cerevisiae	[ui:ycl057w] [pn:saccharolysin protease d:proteinase yscd:oligopeptidase yscd] [gn:prd1:ycl57w] [gtcfc:10.11:7.2] [ec:3.4.24.37] [keggfc:14.1] [sgdgc:6.5.3] [db:gtc-saccharomyces cerevisiae]
CONTIG2081	10631932_c2_8	5382	19485	1455	485	YDR144C	192	4.7(10)-12	Saccharomyces cerevisiae	[ui:ydr144c] [pn:aspartyl protease of the periplasmic space:aspartic proteinase mkc7 precursor] [gn:mkc7:ydr8358] [gtcfc:10.11:1.1:5.2] [ec:3.4.23.-] [keggfc:14.1] [sgdgc:6.5:3:9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3875	23943801_c3_4	5383	19486	675	225	YHR113W	508	8.8(10)-49	Saccharomyces cerevisiae	[ui:yhr113w] [pn:similarity to vacuolar aminopeptidase ape1p:hypothetical 54.2 kd protein in cdc12-orc6 intergenic region] [gtcf:10.11] [keggf:14.2] [sgdfc:6.5.3] [db:gtc-saccharomyces cerevisiae]
CONTIG651	25429661_c2_3	5384	19487	750	250	YHR113W	796	2.7(10)-79	Saccharomyces cerevisiae	[ui:yhr113w] [pn:similarity to vacuolar aminopeptidase ape1p:hypothetical 54.2 kd protein in cdc12-orc6 intergenic region] [gtcf:10.11] [keggf:14.2] [sgdfc:6.5.3] [db:gtc-saccharomyces cerevisiae]
CONTIG3699	26594376_c3_8	5385	19488	870	290	YIL015W	265	3.3(10)-22	Saccharomyces cerevisiae	[ui:yil015w] [pn:barrierpepsin precursor:extracellular] [gn:bar1:ss1] [gtcf:10.11:12.9] [ec:3.4.23.35] [keggf:14.1] [sgdfc:3.3.0:6.5.3] [db:gtc-saccharomyces cerevisiae]
CONTIG3353	5111011_f3_8	5386	19489	564	188	YDL104C	302	5.9(10)-27	Saccharomyces cerevisiae	[ui:ydl104c] [pn:similarity to h.influenzae sialoglycoprotease:gcp:putative protease qri7] [gn:qri7:d2366] [gtcf:10.11] [ec:3.4.24.-] [keggf:14.1] [sgdfc:6.6.0] [db:gtc-saccharomyces cerevisiae]
b1x10133.x	24658450_c3_2	5387	19490	546	182	YDL104C	155	1.3(10)-10	Saccharomyces cerevisiae	[ui:ydl104c] [pn:similarity to h.influenzae sialoglycoprotease:gcp:putative protease qri7] [gn:qri7:d2366] [gtcf:10.11] [ec:3.4.24.-] [keggf:14.1] [sgdfc:6.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5255	15897912_c3_8	5388	19491	513	171	YDR415C	478	1.3(10)-45	Saccharomyces cerevisiae	[ui:ydr415c] [pn:strong similarity to bacterial leucyl aminopeptidase] [gtcf:10.11] [keggf:14.2] [sgdfc:6.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5738	21595160_f2_4	5389	19492	1293	431	YLR299W	575	7.0(10)-56	Saccharomyces cerevisiae	[ui:ytr299w] [pn:gamma-glutamyltransferase, involved in glutathione synthesis] [gn:cis2] [gtcf:10.2:12.8] [keggf:14.2] [sgdfc:1.1.2:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5738	24417207_f3_6	5390	19493	672	224	YLR299W	469	1.2(10)-44	Saccharomyces cerevisiae	[ui:ytr299w] [pn:gamma-glutamyltransferase, involved in glutathione synthesis] [gn:cis2] [gtcf:10.2:12.8] [keggf:14.2] [sgdfc:1.1.2:3.8.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3001	24022812_f3_4	5391	19494	660	220	YMR116C	647	1.6(10)-63	Saccharomyces cerevisiae	[ui:yml16c] [pn:strong similarity to n.crassa cpc2 protein:guanine nucleotide-binding protein beta subunit-like protein] [gn:ym9718] [gtcf:10.2] [keggf:14.2] [sgdfc:1.1.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3001	605055_f1_2	5392	19495	426	142	YMR116C	472	5.7(10)-45	Saccharomyces cerevisiae	[ui:yml16c] [pn:strong similarity to n.crassa cpc2 protein:guanine nucleotide-binding protein beta subunit-like protein] [gn:ym9718] [gtcf:10.2] [keggf:14.2] [sgdfc:1.1.2] [db:gtc-saccharomyces cerevisiae]

CONTIG1120	30484717_c3_3	5393	19496	843	281	YBR142W	288	2.1(10)-24	Saccharomyces cerevisiae	[ui:ybr142w] [pn:atp-dependent rna helicase:atp-dependent rna helicase mak5] [gn:mak5:ybr1119] [gtcf:10.2:10.3] [keggfc:14.2] [sgdfc:4.2.0:4.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5583	24353432_fl_1	5394	19497	1098	366	YBR142W	627	2.2(10)-61	Saccharomyces cerevisiae	[ui:ybr142w] [pn:atp-dependent rna helicase:atp-dependent rna helicase mak5] [gn:mak5:ybr1119] [gtcf:10.2:10.3] [keggfc:14.2] [sgdfc:4.2.0:4.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5583	990677_fl_2	5395	19498	1209	403	YBR142W	629	1.3(10)-61	Saccharomyces cerevisiae	[ui:ybr142w] [pn:atp-dependent rna helicase:atp-dependent rna helicase mak5] [gn:mak5:ybr1119] [gtcf:10.2:10.3] [keggfc:14.2] [sgdfc:4.2.0:4.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2054	24250007_c1_1	5396	19499	336	112	YGL120C	262	1.3(10)-21	Saccharomyces cerevisiae	[ui:ygl120c] [pn:strong similarity to prp22p:putative atp-dependent rna helicase ygl120c] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG902	35792152_fl_1	5397	19500	765	255	YGL120C	1057	5.7(10)-107	Saccharomyces cerevisiae	[ui:ygl120c] [pn:strong similarity to prp22p:putative atp-dependent rna helicase ygl120c] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.9.0] [db:gtc-saccharomyces cerevisiae]
b3x13229.y	6134452_c1_1	5398	19501	513	171	YGL120C	537	8.6(10)-52	Saccharomyces cerevisiae	[ui:ygl120c] [pn:strong similarity to prp22p:putative atp-dependent rna helicase ygl120c] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.9.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5788	23538311_c3_27	5399	19502	1407	469	YHR086W	285	1.0(10)-43	Saccharomyces cerevisiae	[ui:yhr086w] [pn:meiotic recombination protein:nam8 protein] [gn:nam8:mre2] [gtcf:10.2:10.8:12.8] [keggf:14.2] [sgdfc:3.5 0.3 7.0:4.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5094	19728952_c2_12	5400	19503	1488	496	YKL078W	1172	3.7(10)-119	Saccharomyces cerevisiae	[ui:ykl078w] [pn:strong similarity to atp-dependent ma helicases:putative atp-dependent ma helicase ykl078w] [gn:ykl408] [gtcf:10.2] [keggf:14.2] [sgdfc:4.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5094	16598182_c1_10	5401	19504	1128	376	YKL078W	560	2.7(10)-54	Saccharomyces cerevisiae	[ui:ykl078w] [pn:strong similarity to atp-dependent ma helicases:putative atp-dependent ma helicase ykl078w] [gn:ykl408] [gtcf:10.2] [keggf:14.2] [sgdfc:4.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1718	5116262_f1_1	5402	19505	936	312	YKL012W	239	2.2(10)-19	Saccharomyces cerevisiae	[ui:ykl012w] [pn:splicing factor:hypothetical 69.1 kd protein in put3-ccel intergenic region] [gn:prp40-ykl165] [gtcf:10.2] [keggf:14.2] [sgdfc:4.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3526	23634591_f2_2	5403	19506	594	198	YKL012W	132	1.3(10)-16	Saccharomyces cerevisiae	[ui:ykl012w] [pn:splicing factor:hypothetical 69.1 kd protein in put3-ccel intergenic region] [gn:prp40-ykl165] [gtcf:10.2] [keggf:14.2] [sgdfc:4.9.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4950	10351387_f3_5	5404	19507	864	288	YKR024C	509	1.1(10)-48	Saccharomyces cerevisiae	[ui:ykr024c] [pn:similarity to pre-mrna processing protein prp5p:hypothetical 83.3 kd protein in ypt52-gen3 intergenic region] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4950	31818950_f1_3	5405	19508	240	80	YKR024C	142	8.8(10)-9	Saccharomyces cerevisiae	[ui:ykr024c] [pn:similarity to pre-mrna processing protein prp5p:hypothetical 83.3 kd protein in ypt52-gen3 intergenic region] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4950	11757627_f2_4	5406	19509	681	227	YKR024C	275	4.7(10)-23	Saccharomyces cerevisiae	[ui:ykr024c] [pn:similarity to pre-mrna processing protein prp5p:hypothetical 83.3 kd protein in ypt52-gen3 intergenic region] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5796	33992218_c3_20	5407	19510	462	154	YKR024C	355	1.1(10)-31	Saccharomyces cerevisiae	[ui:ykr024c] [pn:similarity to pre-mrna processing protein prp5p:hypothetical 83.3 kd protein in ypt52-gen3 intergenic region] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.9.0] [db:gtc-saccharomyces cerevisiae]
CONTIG421	2844376_f1_1	5408	19511	819	273	YNL286W	203	1.8(10)-16	Saccharomyces cerevisiae	[ui:ynl286w] [pn:cold sensitive u2 snrna suppressor:hypothetical 32.3 kd protein in sec21-mrp110 intergenic region] [gn:cus2:n0549] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.9.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5467	94017_f1_3	5409	19512	276	92	YOR159C	204	1.3(10)-16	Saccharomyces cerevisiae	[ui:yor159c] [pn:strong similarity to human small nuclear ribonucleoprotein e] [gn:smel] [gtcf:10.2:10.9] [keggf:14.2] [sgdf:4.9:4.10.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5618	24038438_c1_18	5410	19513	1905	635	YOR204W	1703	2.1(10)-175	Saccharomyces cerevisiae	[ui:yor204w] [pn:atp-dependent ma helicase:putative atp-dependent ma helicase ded1] [gn:ded1:spp81] [gtcf:10.2:10.7] [keggf:14.2] [sgdf:4.9:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1254	13085062_c2_2	5411	19514	1206	402	YPL060W	517	1.5(10)-54	Saccharomyces cerevisiae	[ui:yp1060w] [pn:strong similarity to mrs2p] [gtcf:10.2] [keggf:14.2] [sgdf:4.9:0] [db:gtc-saccharomyces cerevisiae]
CONTIG5566	34258256_c1_19	5412	19515	393	131	YDR045C	464	4.0(10)-44	Saccharomyces cerevisiae	[ui:ydr045c] [pn:strong similarity to s.acidocaldarius transcription elongation factor tfs] [gtcf:10.2] [keggf:14.2] [sgdf:4.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4966	22070192_c1_7	5413	19516	1185	395	YDR145W	494	2.7(10)-47	Saccharomyces cerevisiae	[ui:ydr145w] [pn:tfid subunit:tbp-associated factor] [gn:taf61] [gtcf:10.2] [keggf:14.2] [sgdf:4.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5705	9978402_c1_14	5414	19517	1551	517	YDR145W	338	2.2(10)-30	Saccharomyces cerevisiae	[ui:ydr145w] [pn:tfid subunit:tbp-associated factor] [gn:taf61] [gtcf:10.2] [keggf:14.2] [sgdf:4.8.1] [db:gtc-saccharomyces cerevisiae]

CONTIG2805	23631531_c2_6	5415	19518	726	242	YDR167W	419	2.3(10)-39	Saccharomyces cerevisiae	[ui:ydr167w] [pn:tfid subunit:tbp-associated factor, 23 kd] [gn:taf23] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG1627	4096062_c3_4	5416	19519	501	167	YGL244W	197	4.5(10)-15	Saccharomyces cerevisiae	[ui:ygl244w] [pn:involved in tata site selection by tbp:hypothetical 54.6 kd protein in pde1-cse1 intergenic region] [gn:rtf1:hra458] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3430	25478412_c2_4	5417	19520	1281	427	YGL244W	250	4.5(10)-26	Saccharomyces cerevisiae	[ui:ygl244w] [pn:involved in tata site selection by tbp:hypothetical 54.6 kd protein in pde1-cse1 intergenic region] [gn:rtf1:hra458] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4359	29428312_f2_4	5418	19521	1005	335	YML015C	128	4.2(10)-11	Saccharomyces cerevisiae	[ui:ym1015c] [pn:tfid subunit:tbp-associated factor, 40kd] [gn:taf40] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3736	4062655_f2_3	5419	19522	1320	440	YMR227C	99	0.07199	Saccharomyces cerevisiae	[ui:ymr227c] [pn:tfid subunit:tbp-associated factor, 67 kd] [gn:taf67] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG5817	9929701_c2_50	5420	19523	1248	416	YMR227C	91	0.00018	Saccharomyces cerevisiae	[ui:ymr227c] [pn:tfid subunit:tbp-associated factor, 67 kd] [gn:taf67] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.1] [db:gtc-saccharomyces cerevisiae]

CONTIG5817	24313753_c3_58	5421	19524	201	67	YMR227C	106	4.7(10)-5	Saccharomyces cerevisiae	[ui:ymr227c] [pn:tfiid subunit:tbp-associated factor, 67 kd] [gn:taf67] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG3717	1257677_fl_2	5422	19525	339	113	YPL046C	159	8.4(10)-12	Saccharomyces cerevisiae	[ui:yp046c] [pn:strong similarity to human dna-directed rna polymerase ii elongation factor siii p15 subunit] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.1] [db:gtc-saccharomyces cerevisiae]
CONTIG4645	5079530_c3_8	5423	19526	1356	452	YAR003W	522	6.0(10)-80	Saccharomyces cerevisiae	[ui:yar003w] [pn:similarity to human rb protein binding protein:hypothetical trp-aspartate repeats containing protein in tfc3-rfa1 intergenic region] [gn:fun16] [gtcf:10.2:12.8] [keggfc:14.2] [sgdfc:3.8.0:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3762	241637_f3_3	5424	19527	1026	342	YBL066C	141	1.3(10)-9	Saccharomyces cerevisiae	[ui:ybl066c] [pn:putative transcription factor:putative 118.2 kd transcriptional regulatory protein in ubp13-kip1 intergenic region] [gn:sef1:ybl0501:ybl0526] [gtcf:10.2:12.15] [keggfc:14.2] [sgdfc:3.4.0:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4782	35392050_c3_12	5425	19528	1626	542	YBL066C	652	5.2(10)-90	Saccharomyces cerevisiae	[ui:ybl066c] [pn:putative transcription factor:putative 118.2 kd transcriptional regulatory protein in ubp13-kip1 intergenic region] [gn:sef1:ybl0501:ybl0526] [gtcf:10.2:12.15] [keggfc:14.2] [sgdfc:3.4.0:4.8.2] [db:gtc-saccharomyces cerevisiae]

b9x11s19.x	21517807_c2_2	5426	19529	531	177	YBL066C	481	7.7(10)-45	Saccharomyces cerevisiae	[ui:ybl066c] [pn:putative transcription factor:putative 118.2 kd transcriptional regulatory protein in ubp13-kip1 intergenic region] [gn:sef1:ybl0501:ybl0526] [gtcf:10.2:12.15] [keggfc:14.2] [sgdgc:3.4.0:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5117	24015900_c1_7	5427	19530	2202	734	YBL052C	877	6.9(10)-88	Saccharomyces cerevisiae	[ui:ybl052c] [pn:silencing protein:hypothetical 97.6 kd protein in ptc3-secl7 intergenic region] [gn:sas3:ybl0515:ybl0507] [gtcf:10.2:12.9] [keggfc:14.2] [sgdgc:3.3.0:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5690	5313390_c2_22	5428	19531	2916	972	YBR033W	99	0.25	Saccharomyces cerevisiae	[ui:ybr033w] [pn:weak similarity to transcription factors:putative 103.4 kd transcriptional regulatory protein in rpl2-odp1 intergenic region] [gn:ybr0318] [gtcf:10.2] [keggfc:14.2] [sgdgc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5253	23645200_f1_1	5429	19532	948	316	YBR061C	929	2.1(10)-93	Saccharomyces cerevisiae	[ui:ybr061c] [pn:similarity to e.coli ftsj protein:hypothetical 34.7 kd protein in orc2-tip1 intergenic region] [gn:ybr0527] [gtcf:10.2] [keggfc:14.2] [sgdgc:4.8.2] [db:gtc-saccharomyces cerevisiae]

CONTIG4558	34239382_f3_7	5430	19533	447	149	YBR215W	154	3.5(10)-10	Saccharomyces cerevisiae	[ui:ybr215w] [pn:cell cycle regulatory protein:histone promoter control 2 protein] [gn:hpc2:ybr1503] [gtcf:10.2:12.8] [keggf:14.2] [sgdf:3.8.0:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4332	30251343_c1_8	5431	19534	1452	484	YBR245C	1761	1.5(10)-181	Saccharomyces cerevisiae	[ui:ybr245c] [pn:strong similarity to snf2/swi2 dna binding regulatory protein:hypothetical 132.7 kd helicase in alg7-enp1 intergenic region] [gn:ybr1633] [gtcf:10.2] [keggf:14.2] [sgdf:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4332	21642001_c1_7	5432	19535	330	110	YBR245C	146	5.7(10)-9	Saccharomyces cerevisiae	[ui:ybr245c] [pn:strong similarity to snf2/swi2 dna binding regulatory protein:hypothetical 132.7 kd helicase in alg7-enp1 intergenic region] [gn:ybr1633] [gtcf:10.2] [keggf:14.2] [sgdf:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4551	26384826_f2_2	5433	19536	858	286	YBR245C	490	1.0(10)-45	Saccharomyces cerevisiae	[ui:ybr245c] [pn:strong similarity to snf2/swi2 dna binding regulatory protein:hypothetical 132.7 kd helicase in alg7-enp1 intergenic region] [gn:ybr1633] [gtcf:10.2] [keggf:14.2] [sgdf:4.8.2] [db:gtc-saccharomyces cerevisiae]

CONTIG5642	10188800_c2_19	5434	19537	669	223	YCR020C	185	2.1(10)-21	Saccharomyces cerevisiae	[ui:ycr020c] [pn:similarity to regulatory protein:pet18 protein] [gn:pet18:hi2:ycr20c] [gtcf:10.2] [keggf:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2578	10657875_c2_5	5435	19538	1395	465	YDL153C	381	5.7(10)-64	Saccharomyces cerevisiae	[ui:ydl153c] [pn:involved in silencing] [gn:sas10] [gtcf:10.2] [keggf:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4067	26210886_c3_4	5436	19539	963	321	YDR017C	430	6.4(10)-51	Saccharomyces cerevisiae	[ui:ydr017c] [pn:potential transcription factor of the bzip type] [gn:kcs1] [gtcf:10.2] [keggf:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5453	4329067_c2_23	5437	19540	1476	492	YDR026C	273	1.0(10)-25	Saccharomyces cerevisiae	[ui:ydr026c] [pn:strong similarity to dna-binding protein reb1p] [gtcf:10.2] [keggf:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2433	21972625_c3_4	5438	19541	705	235	YDR334W	627	4.2(10)-60	Saccharomyces cerevisiae	[ui:ydr334w] [pn:similarity to nuclear sth1p, snf2p and related proteins] [gtcf:10.2] [keggf:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4520	1458582_c3_7	5439	19542	2697	899	YDR334W	1462	1.3(10)-178	Saccharomyces cerevisiae	[ui:ydr334w] [pn:similarity to nuclear sth1p, snf2p and related proteins] [gtcf:10.2] [keggf:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5708	4787512_c2_24	5440	19543	3969	1323	YDR464W	122	0.0023	Saccharomyces cerevisiae	[ui:ydr464w] [pn:negative regulator of prp3 and prp4 gene expression:protein] [gn:spp41] [gtcf:10.2] [keggf:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]

CONTIG3037	547083_f2_2	5441	19544	1215	405	YEL056W	473	2.7(10)-65	Saccharomyces cerevisiae	[ui:yel056w] [pn:subunit of the major yeast histone acetyltransferase:hypothetical trp-asp repeats containing protein in pcm1-rp115b intergenic region] [gn:hat2] [gtcf:10.2:10.7] [keggfc:14.2] [sgdfc:4.8.2:6.3.0.9.2.0] [db:gtc-saccha]
CONTIG5752	13751312_f2_9	5442	19545	1497	499	YEL056W	494	2.7(10)-47	Saccharomyces cerevisiae	[ui:yel056w] [pn:subunit of the major yeast histone acetyltransferase:hypothetical trp-asp repeats containing protein in pcm1-rp115b intergenic region] [gn:hat2] [gtcf:10.2:10.7] [keggfc:14.2] [sgdfc:4.8.2:6.3.0.9.2.0] [db:gtc-saccha]
CONTIG5770	14459375_f3_15	5443	19546	1278	426	YER027C	472	7.7(10)-78	Saccharomyces cerevisiae	[ui:yer027c] [pn:glucose repression protein:glucose repression protein gal83:spm1 protein] [gn:gal83:spm1] [gtcf:10.2:12.13] [keggfc:14.2] [sgdfc:1.5.2.4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1916	24006261_f1_1	5444	19547	1332	444	YER164W	1651	6.5(10)-170	Saccharomyces cerevisiae	[ui:yer164w] [pn:transcriptional regulator:hypothetical 168.2 kd protein in rad4-pab1 intergenic region] [gn:chd1:sygp-orf4] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]

CONTIG241	1204413_c3_2	5445	19548	642	214	YER164W	803	5.5(10)-79	Saccharomyces cerevisiae	[ui:yer164w] [pn:transcriptional regulator:hypothetical 168.2 kd protein in rad4-pab1 intergenic region] [gn:chd1:sygp-orf4] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3287	31942_c3_7	5446	19549	1254	418	YER164W	365	3.6(10)-56	Saccharomyces cerevisiae	[ui:yer164w] [pn:transcriptional regulator:hypothetical 168.2 kd protein in rad4-pab1 intergenic region] [gn:chd1:sygp-orf4] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3940	19571965_c3_15	5447	19550	1053	351	YER169W	336	1.5(10)-29	Saccharomyces cerevisiae	[ui:yer169w] [pn:similarity to human retinoblastoma binding protein 2:putative 90.2 kd zinc finger protein in cca1-adk2 intergenic region] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2457	24016507_c3_3	5448	19551	243	81	YGL221C	142	1.5(10)-9	Saccharomyces cerevisiae	[ui:ygl221c] [pn:ngg1p-interacting factor 3:hypothetical 31.9 kd protein in gog5-clg1 intergenic region] [gn:nif3] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3428	24016507_c1_3	5449	19552	222	74	YGL221C	139	3.2(10)-9	Saccharomyces cerevisiae	[ui:ygl221c] [pn:ngg1p-interacting factor 3:hypothetical 31.9 kd protein in gog5-clg1 intergenic region] [gn:nif3] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]

b1x12535.y	658431_c3_5	5450	19553	306	102	YGL221C	178	1.1(10)-13	Saccharomyces cerevisiae	[ui:ygl221c] [pn:ngg1p-interacting factor 3:hypothetical 31.9 kd protein in gog5-clg1 intergenic region] [gn:nif3] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
b3x19292.x	19625262_c1_3	5451	19554	699	233	YGL181W	404	9.1(10)-38	Saccharomyces cerevisiae	[ui:ygl181w] [pn:transcription factor of the gcs1p/glo3p/sps18p family:gts1 protein:lsl1 protein] [gn:gts1:lsl1] [gtcf:10.2:12.8:13.2] [keggfc:14.2] [sgdfc:3.2.0:3.8.0:4.8.2:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5777	4694055_c3_26	5452	19555	4185	1395	YGL150C	1758	1.3(10)-261	Saccharomyces cerevisiae	[ui:ygl150c] [pn:similarity to snf2p and human snf2alpha:hypothetical 171.5 kd helicase in lys5-aro2 intergenic region] [gn:g1880] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3283	1934656_c3_3	5453	19556	1707	569	YGL073W	415	2.5(10)-52	Saccharomyces cerevisiae	[ui:ygl073w] [pn:heat shock factor protein:hsf:heat shock transcription factor:hstf] [gn:hsf1] [gtcf:12.7:10.2:13.2] [keggfc:14.2] [sgdfc:4.8.2:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4623	24350010_c2_9	5454	19557	1491	497	YGL073W	93	0.46	Saccharomyces cerevisiae	[ui:ygl073w] [pn:heat shock factor protein:hsf:heat shock transcription factor:hstf] [gn:hsf1] [gtcf:12.7:10.2:13.2] [keggfc:14.2] [sgdfc:4.8.2:11.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG489	787510_c3_3	5455	19558	624	208	YGR097W	90	0.37	Saccharomyces cerevisiae	[ui:ygr097w] [pn:involved in skn7p-dependent transcription:protein] [gn:ask10] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4474	21698426_c3_8	5456	19559	1149	383	YGR100W	586	2.2(10)-56	Saccharomyces cerevisiae	[ui:ygr100w] [pn:mac1p interacting protein:mic1 protein] [gn:mic1:g5717] [gtcf:10.2:13.2] [keggfc:14.2] [sgdfc:4.8.2:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4474	11223943_c2_6	5457	19560	1083	361	YGR100W	1222	1.8(10)-124	Saccharomyces cerevisiae	[ui:ygr100w] [pn:mac1p interacting protein:mic1 protein] [gn:mic1:g5717] [gtcf:10.2:13.2] [keggfc:14.2] [sgdfc:4.8.2:11.1.0] [db:gtc-saccharomyces cerevisiae]
b9x13m30.y	4407157_f2_1	5458	19561	297	99	YGR100W	110	3.2(10)-5	Saccharomyces cerevisiae	[ui:ygr100w] [pn:mac1p interacting protein:mic1 protein] [gn:mic1:g5717] [gtcf:10.2:13.2] [keggfc:14.2] [sgdfc:4.8.2:11.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4300	6145055_c3_12	5459	19562	1908	636	YHR178W	836	3.6(10)-88	Saccharomyces cerevisiae	[ui:yhr178w] [pn:sin3 binding protein:putative 83.5 kd transcriptional regulatory protein in eno2-oye2 intergenic region] [gn:sib5] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4379	9845317_f1_1	5460	19563	2016	672	YHR178W	91	0.65	Saccharomyces cerevisiae	[ui:yhr178w] [pn:sin3 binding protein:putative 83.5 kd transcriptional regulatory protein in eno2-oye2 intergenic region] [gn:sib5] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]

CONTIG5812	13759657_f3_18	5461	19564	711	237	YHR178W	103	0.0071	Saccharomyces cerevisiae	[ui:yhr178w] [pn:sin3 binding protein:putative 83.5 kd eno2-oye2 intergenic region] [gn:stb5] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1667	34385005_f2_1	5462	19565	1227	409	YIL130W	99	0.063	Saccharomyces cerevisiae	[ui:yil130w] [pn:similarity to put3p and to hypothetical protein yj1206c:putative 108.8 kd transcriptional regulatory protein in fkh1-sth1 intergenic region] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2486	190937_f1_1	5463	19566	588	196	YIL130W	99	0.016	Saccharomyces cerevisiae	[ui:yil130w] [pn:similarity to put3p and to hypothetical protein yj1206c:putative 108.8 kd transcriptional regulatory protein in fkh1-sth1 intergenic region] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3929	26615877_c1_1	5464	19567	2190	730	YIL130W	171	3.7(10)-9	Saccharomyces cerevisiae	[ui:yil130w] [pn:similarity to put3p and to hypothetical protein yj1206c:putative 108.8 kd transcriptional regulatory protein in fkh1-sth1 intergenic region] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]

CONTIG4508	11718875_c2_3	5465	19568	1605	535	YIL130W	130	6.0(10)-5	Saccharomyces cerevisiae	[ui:yil130w] [pn:similarity to put3p and to hypothetical protein yj1206c:putative 108.8 kd transcriptional regulatory protein in fkh1-sth1 intergenic region] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4575	10172526_c1_7	5466	19569	792	264	YIL130W	205	2.2(10)-15	Saccharomyces cerevisiae	[ui:yil130w] [pn:similarity to put3p and to hypothetical protein yj1206c:putative 108.8 kd transcriptional regulatory protein in fkh1-sth1 intergenic region] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
b3x17449.y	24412675_c3_4	5467	19570	327	109	YIL130W	132	1.3(10)-7	Saccharomyces cerevisiae	[ui:yil130w] [pn:similarity to put3p and to hypothetical protein yj1206c:putative 108.8 kd transcriptional regulatory protein in fkh1-sth1 intergenic region] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4784	32229813_f2_6	5468	19571	792	264	YIL050W	223	9.3(10)-34	Saccharomyces cerevisiae	[ui:yil050w] [pn:similarity to n.crassa regulatory protein preg:+-hypothetical 32.0 kd protein in gppl-syl1 intergenic region] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]

CONTIG2883	10579552_f3_4	5469	19572	321	107	YJL115W	277	2.6(10)-24	Saccharomyces cerevisiae	[ui:yjl115w] [pn:anti-silencing protein:anti-silencing protein 1] [gn:asf1:j0755] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4945	25665938_f2_1	5470	19573	1578	526	YJL115W	113	0.00059	Saccharomyces cerevisiae	[ui:yjl115w] [pn:anti-silencing protein:anti-silencing protein 1] [gn:asf1:j0755] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1122	7320285_c2_2	5471	19574	723	241	YJR032W	547	6.5(10)-53	Saccharomyces cerevisiae	[ui:yjr032w] [pn:member of the cyclophilin family:peptidyl-prolyl cis-trans isomerase cyp7:ppiase:rotamase] [gn:cpr7:j1585] [gtcf:10.2:10.5:10.7:12.7:12.8] [ec:5.2.1.8] [keggfc:14.1] [sgdfc:3.1.0:4.8.2:6.1.0] [db:gtc-saccharomyces ce]
CONTIG5620	7893_f1_2	5472	19575	1221	407	YJR032W	599	2.2(10)-72	Saccharomyces cerevisiae	[ui:yjr032w] [pn:member of the cyclophilin family:peptidyl-prolyl cis-trans isomerase cyp7:ppiase:rotamase] [gn:cpr7:j1585] [gtcf:10.2:10.5:10.7:12.7:12.8] [ec:5.2.1.8] [keggfc:14.1] [sgdfc:3.1.0:4.8.2:6.1.0] [db:gtc-saccharomyces ce]
CONTIG3852	36382953_f3_1	5473	19576	1524	508	YJR119C	132	2.7(10)-12	Saccharomyces cerevisiae	[ui:yjr119c] [pn:similarity to human retinoblastoma binding protein 2:hypothetical 85.0 kd protein in nmf1-atp2 intergenic region] [gn:j2035] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]

CONTIG5804	20343762_f2_19	5474	19577	393	131	YJR119C	172	5.2(10)-12	Saccharomyces cerevisiae	[ui:yjr119c] [pn:similarity to human retinoblastoma binding protein 2:hypothetical 85.0 kd protein in nnf1-ap2 intergenic region] [gn:j2035] [gtcf:10.2] [keggf:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5804	20704760_f2_20	5475	19578	1800	600	YJR119C	806	2.2(10)-80	Saccharomyces cerevisiae	[ui:yjr119c] [pn:similarity to human retinoblastoma binding protein 2:hypothetical 85.0 kd protein in nnf1-ap2 intergenic region] [gn:j2035] [gtcf:10.2] [keggf:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5322	24228466_f2_4	5476	19579	660	220	YKL185W	295	1.8(10)-25	Saccharomyces cerevisiae	[ui:ykl185w] [pn:negative regulator of ho expression:hypothetical 65.7 kd protein in mtr2-ord1 intergenic region] [gn:ash1] [gtcf:10.2:12.9] [keggf:14.2] [sgdfc:3.0:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1694	33484567_c1_4	5477	19580	984	328	YKL072W	90	0.5	Saccharomyces cerevisiae	[ui:ykl072w] [pn:sin3 binding protein:hypothetical 88.8 kd protein in lhs1-nup100 intergenic region] [gn:stb6:ykl352] [gtcf:10.2] [keggf:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]

b3x13540.y	116379_c1_2	5478	19581	444	148	YKL070W	213	1.6(10)-17	Saccharomyces cerevisiae	[ui:ykl070w] [pn:similarity to b.subtilis transcriptional regulatory protein:hypothetical 19.8 kd protein in lls1-nup100 intergenic region] [gn:ykl343] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG1623	4490650_f2_2	5479	19582	798	266	YKR036C	129	1.5(10)-5	Saccharomyces cerevisiae	[ui:ykr036c] [pn:ccr4 associated factor:hypothetical trp-asp repeats containing protein in dal80-gap1 intergenic region] [gn:caf4] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2785	1203385_f2_3	5480	19583	648	216	YKR036C	129	6.0(10)-6	Saccharomyces cerevisiae	[ui:ykr036c] [pn:ccr4 associated factor:hypothetical trp-asp repeats containing protein in dal80-gap1 intergenic region] [gn:caf4] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3407	35580275_f2_2	5481	19584	312	104	YKR064W	104	0.00012	Saccharomyces cerevisiae	[ui:ykr064w] [pn:weak similarity to transcription factors:putative 101.8 kd transcriptional regulatory protein in las1-ccp1 intergenic region] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]

CONTIG4938	25596942_f3_4	5482	19585	528	176	YLR136C	239	2.7(10)-20	Saccharomyces cerevisiae	[ui:ylr136c] [pn:member of the inducible cecch zinc-finger family:zinc finger protein cth2:ytis11 protein] [gn:cth2:its11:19606] [gtcfc:10.2] [keggfc:14.2] [sgdgc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4311	23681561_f3_5	5483	19586	1224	408	YLR216C	943	7.0(10)-95	Saccharomyces cerevisiae	[ui:ylr216c] [pn:member of the cyclophilin family:peptidyl-prolyl cis-trans isomerase cyp6:ppiase:rotamase] [gn:cpr6:l8167] [gtcfc:10.2:10.5:10.7:12.7:14.1] [ec:5.2.1.8] [keggfc:14.1] [sgdgc:4.8.2:6.1.0:9.2.0] [db:gtc-saccharomyces ce
CONTIG3802	266942_c1_8	5484	19587	759	253	YLR228C	204	2.2(10)-15	Saccharomyces cerevisiae	[ui:ylr228c] [pn:strong similarity to ydr213w, weak similarity to lys14p] [gtcfc:10.2] [keggfc:14.2] [sgdgc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4763	6370753_f2_3	5485	19588	1212	404	YLR228C	917	4.0(10)-92	Saccharomyces cerevisiae	[ui:ylr228c] [pn:strong similarity to ydr213w, weak similarity to lys14p] [gtcfc:10.2] [keggfc:14.2] [sgdgc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4218	21517037_f3_2	5486	19589	1152	384	YML081W	280	3.2(10)-23	Saccharomyces cerevisiae	[ui:yml081w] [pn:strong similarity to zms1 protein] [gtcfc:10.2] [keggfc:14.2] [sgdgc:4.8.2] [db:gtc-saccharomyces cerevisiae]

CONTIG4755	25978317_β_2	5487	19590	2022	674	YML081W	373	4.9(10)-31	Saccharomyces cerevisiae	[ui:yml081w] [pn:strong similarity to zms1 protein] [gtcf:10.2] [keggf:14.2] [sgdf:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG2923	34406717_β_4	5488	19591	1263	421	YMR019W	183	1.5(10)-19	Saccharomyces cerevisiae	[ui:ymr019w] [pn:sin3 binding protein:putative 109.8 kd sok2-fms1 intergenic region] [gn:stb4:ym9711] [gtcf:10.2] [keggf:14.2] [sgdf:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4039	3164050_c2_7	5489	19592	1110	370	YMR019W	111	0.00359	Saccharomyces cerevisiae	[ui:ymr019w] [pn:sin3 binding protein:putative 109.8 kd sok2-fms1 intergenic region] [gn:stb4:ym9711] [gtcf:10.2] [keggf:14.2] [sgdf:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4390	26378336_c3_10	5490	19593	939	313	YMR019W	126	3.0(10)-5	Saccharomyces cerevisiae	[ui:ymr019w] [pn:sin3 binding protein:putative 109.8 kd sok2-fms1 intergenic region] [gn:stb4:ym9711] [gtcf:10.2] [keggf:14.2] [sgdf:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4765	4163211_c3_8	5491	19594	789	263	YMR019W	194	3.3(10)-14	Saccharomyces cerevisiae	[ui:ymr019w] [pn:sin3 binding protein:putative 109.8 kd sok2-fms1 intergenic region] [gn:stb4:ym9711] [gtcf:10.2] [keggf:14.2] [sgdf:4.8.2] [db:gtc-saccharomyces cerevisiae]

b9x13233.x	20806887_c3_1	5492	19595	621	207	YMR053C	165	3.7(10)-11	Saccharomyces cerevisiae	[ui:ymr053c] [pn:sn3p binding protein:stb2 protein] [gn:stb2:ym9796] [gtcf:10.2] [keggf:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5814	34173260_cl_36	5493	19596	1077	359	YMR127C	524	2.3(10)-58	Saccharomyces cerevisiae	[ui:yml127c] [pn:involved in silencing at hmr:sas2 protein] [gn:sas2:ym9553] [gtcf:10.2:12.8:12.9] [keggf:14.2] [sgdfc:3.0:3.8:0.4:8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5741	10634655_f3_8	5494	19597	768	256	YNL107W	282	7.5(10)-38	Saccharomyces cerevisiae	[ui:ynl107w] [pn:similarity to human af-9 protein:hypothetical 26.0 kd protein in cyb5-leu4 intergenic region] [gn:n1966] [gtcf:10.2] [keggf:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5142	956251_c2_6	5495	19598	357	119	YOL133W	388	4.5(10)-36	Saccharomyces cerevisiae	[ui:yol133w] [pn:similarity to lotus ring-finger protein] [gtcf:10.2] [keggf:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3634	21678177_cl_7	5496	19599	1020	340	YOL068C	631	5.5(10)-94	Saccharomyces cerevisiae	[ui:yol068c] [pn:silencing protein:protein] [gn:hst1] [gtcf:10.2:12.9] [keggf:14.2] [sgdfc:3.0:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5551	962637_fl_3	5497	19600	1644	548	YOL055C	462	9.0(10)-55	Saccharomyces cerevisiae	[ui:yol055c] [pn:weak similarity to bacterial transcription factors] [gtcf:10.2] [keggf:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]

CONTIG4179	2775332_f2_1	5498	19601	1467	489	YOR025W	838	9.4(10)-84	Saccharomyces cerevisiae	[ui:yor025w] [pn:silencing protein:hst3 protein] [gn:hst3:or26] [gtcf:10.2] [keggfc:14.2] [sgdgc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3722	14642938_f3_2	5499	19602	1827	609	YOR304W	1781	1.1(10)-183	Saccharomyces cerevisiae	[ui:yor304w] [pn:strong similarity to human snf2p homolog] [gtcf:10.2] [keggfc:14.2] [sgdgc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG4332	22285135_c2_10	5500	19603	237	79	YOR304W	155	6.0(10)-10	Saccharomyces cerevisiae	[ui:yor304w] [pn:strong similarity to human snf2p homolog] [gtcf:10.2] [keggfc:14.2] [sgdgc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3389	9960258_c2_17	5501	19604	276	92	YOR304W	225	2.1(10)-17	Saccharomyces cerevisiae	[ui:yor304w] [pn:strong similarity to human snf2p homolog] [gtcf:10.2] [keggfc:14.2] [sgdgc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3389	1302_c2_16	5502	19605	273	91	YOR304W	142	1.5(10)-8	Saccharomyces cerevisiae	[ui:yor304w] [pn:strong similarity to human snf2p homolog] [gtcf:10.2] [keggfc:14.2] [sgdgc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG3787	34087807_c2_8	5503	19606	852	284	YPL015C	663	3.2(10)-65	Saccharomyces cerevisiae	[ui:ypl015c] [pn:similarity to hst1p and sir2p:hst2 protein] [gn:hst2:ipa2c] [gtcf:10.2] [keggfc:14.2] [sgdgc:4.8.2] [db:gtc-saccharomyces cerevisiae]

CONTIG5531	34462782_f3_20	5504	19607	795	265	YPR115W	118	4.2(10)-9	Saccharomyces cerevisiae	[ui:ypr115w] [pn:similarity to probable transcription factor ask10p. and to hypothetical proteins ynl047c and yil105c] [gtcf:10.2] [keggc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5531	24844186_f2_14	5505	19608	1182	394	YPR115W	136	9.0(10)-6	Saccharomyces cerevisiae	[ui:ypr115w] [pn:similarity to probable transcription factor ask10p. and to hypothetical proteins ynl047c and yil105c] [gtcf:10.2] [keggc:14.2] [sgdfc:4.8.2] [db:gtc-saccharomyces cerevisiae]
CONTIG5468	3943927_c1_15	5506	19609	1476	492	YAL013W	159	4.2(10)-9	Saccharomyces cerevisiae	[ui:yal013w] [pn:regulator of phospholipid metabolism.depl protein] [gn:depl:fun54] [gtcf:10.2] [keggc:14.2] [sgdfc:1.6.4:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2498	3937516_c2_4	5507	19610	852	284	YGL162W	108	0.00046	Saccharomyces cerevisiae	[ui:ygl162w] [pn:hypoxic protein involved in sterol uptake:probable sterol carrier] [gn:sut1:g1828] [gtcf:10.2] [keggc:14.2] [sgdfc:1.6.4] [db:gtc-saccharomyces cerevisiae]
CONTIG5619	875463_f2_5	5508	19611	513	171	YJL096W	220	2.8(10)-18	Saccharomyces cerevisiae	[ui:yjl096w] [pn:putative regulator of purine and/or pyrimidine biosynthesis:hypothetical 25.4 kd protein in sap185-bck1 intergenic region] [gn:j0904] [gtcf:10.2] [keggc:14.2] [sgdfc:1.3.5] [db:gtc-saccharomyces cerevisiae]

CONTIG5357	20895052_c1_14	5509	19612	702	234	YOL110W	152	2.5(10)-10	Saccharomyces cerevisiae	[ui:yol110w] [pn:ras suppressor:ras modification protein shr5] [gn:shr5:hrc237] [gtcf:10.2:12.13:12.8:13.2] [keggfc:14.2] [sgdgc:1.3.5:1.5.2.3.10.0:10.4.8] [db:gtc-saccharomyces cerevisiae]
CONTIG1003	24251676_c2_1	5510	19613	798	266	YOR101W	550	3.1(10)-53	Saccharomyces cerevisiae	[ui:yor101w] [pn:gtp-binding protein:ras-like protein 1] [gn:ras1:yor3205w] [gtcf:10.2:11.1:12.13:12.8] [keggfc:13.1] [sgdgc:1.3.5:1.5.2.3.10.0:9.1.0:10.4.4:11.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3766	3908311_fl_1	5511	19614	996	332	YOR101W	221	1.1(10)-17	Saccharomyces cerevisiae	[ui:yor101w] [pn:gtp-binding protein:ras-like protein 1] [gn:ras1:yor3205w] [gtcf:10.2:11.1:12.13:12.8] [keggfc:13.1] [sgdgc:1.3.5:1.5.2.3.10.0:9.1.0:10.4.4:11.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5802	4803441_f2_17	5512	19615	567	189	YOR101W	352	3.0(10)-32	Saccharomyces cerevisiae	[ui:yor101w] [pn:gtp-binding protein:ras-like protein 1] [gn:ras1:yor3205w] [gtcf:10.2:11.1:12.13:12.8] [keggfc:13.1] [sgdgc:1.3.5:1.5.2.3.10.0:9.1.0:10.4.4:11.5.0] [db:gtc-saccharomyces cerevisiae]

b9x11m02.x	14068917_c2_5	5513	19616	711	237	YOR101W	437	2.8(10)-41	Saccharomyces cerevisiae	[ui:yor101w] [pn:gtp-binding protein:ras-like protein 1] [gn:ras1.yor3205w] [gtcf:10.2:11.1:12.13:12.8] [keggfc:13.1] [sgdgc:1.3.5:1.5.2:3.10.0:9.1.0:10.4.4:11.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1745	24001542_c3_6	5514	19617	648	216	YFR004W	220	2.8(10)-18	Saccharomyces cerevisiae	[ui:yfr004w] [pn:strong similarity to s.pombe pad1 protein:protein] [gn:mpr1] [gtcf:10.2:10.6] [keggfc:14.2] [sgdgc:4.0:4.5.0] [db:gtc-saccharomyces cerevisiae]
b2x19164.x	33385_c1_6	5515	19618	783	261	YFR004W	894	1.1(10)-89	Saccharomyces cerevisiae	[ui:yfr004w] [pn:strong similarity to s.pombe pad1 protein:protein] [gn:mpr1] [gtcf:10.2:10.6] [keggfc:14.2] [sgdgc:4.0:4.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5668	163188_f1_1	5516	19619	1893	631	YBR238C	438	2.0(10)-39	Saccharomyces cerevisiae	[ui:ybr238c] [pn:strong similarity to general chromatin factor spt16p:hypothetical 83.7 kd protein in prp5-alg7 intergenic region] [gn:ybr1608] [gtcf:10.2:12.8] [keggfc:14.2] [sgdgc:3.8.0:4.8.3] [db:gtc-saccharomyces cerevisiae]
CONTIG4750	15134650_c2_7	5517	19620	2280	760	YBR212W	470	4.2(10)-79	Saccharomyces cerevisiae	[ui:ybr212w] [pn:glucose-repressible ma-binding protein:negative growth regulatory protein ngr1:ma-binding protein rbp1] [gn:ngl1.ybr1459] [gtcf:10.2:12.8] [keggfc:14.2] [sgdgc:3.1.0:4.12.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2397	9939050_c2_3	5518	19621	894	298	YBR233W	195	5.7(10)-15	Saccharomyces cerevisiae	[ui:ybr233w] [pn:similarity to human hnmp-e1 protein:hypothetical 45.8 kd protein in pcs60-abd1 intergenic region] [gn:ybr1531] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5481	22479187_c1_12	5519	19622	966	322	YBR233W	347	1.0(10)-31	Saccharomyces cerevisiae	[ui:ybr233w] [pn:similarity to human hnmp-e1 protein:hypothetical 45.8 kd protein in pcs60-abd1 intergenic region] [gn:ybr1531] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4607	10737577_f3_6	5520	19623	435	145	YCL033C	310	8.4(10)-28	Saccharomyces cerevisiae	[ui:ycl033c] [pn:similarity to m.capricolum transcription repressor:hypothetical 19.3 kd protein in ste50 5"region] [gn:ycl33c] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2363	13710252_c3_7	5521	19624	477	159	YCR004C	504	2.2(10)-48	Saccharomyces cerevisiae	[ui:ycr004c] [pn:strong similarity to s. pombe protein obr1:hypothetical 26.4 kd protein in cdc10-cit2 intergenic region] [gn:ycp4:ycr4c:ycr042] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]

CONTIG434	22712776_c2_2	5522	19625	813	271	YCR004C	598	2.5(10)-58	Saccharomyces cerevisiae	[ui:ycr004c] [pn:strong similarity to s. pombe protein obr1:hypothetical 26.4 kd protein in cdc10-cit2 intergenic region] [gn:ycp4:ycr4c:ycr042] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5438	21956281_c2_18	5523	19626	681	227	YCR004C	610	1.3(10)-59	Saccharomyces cerevisiae	[ui:ycr004c] [pn:strong similarity to s. pombe protein obr1:hypothetical 26.4 kd protein in cdc10-cit2 intergenic region] [gn:ycp4:ycr4c:ycr042] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5438	20509375_f3_10	5524	19627	768	256	YCR004C	566	6.2(10)-55	Saccharomyces cerevisiae	[ui:ycr004c] [pn:strong similarity to s. pombe protein obr1:hypothetical 26.4 kd protein in cdc10-cit2 intergenic region] [gn:ycp4:ycr4c:ycr042] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5343	6735005_c2_16	5525	19628	420	140	YCR087C-A	243	1.1(10)-20	Saccharomyces cerevisiae	[ui:ycr087c-a] [pn:nucleic acid-binding protein:hypothetical 17.7 kd protein in abp1 5' region] [gn:ycrx16c] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4385	24617258_fl_1	5526	19629	843	281	YDL051W	167	1.7(10)-12	Saccharomyces cerevisiae	[ui:ydl051w] [pn:ma binding protein:la protein homolog] [gn:lah1:lhpl:yla1] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3713	22307888_c3_10	5527	19630	1146	382	YDL031W	923	9.3(10)-93	Saccharomyces cerevisiae	[ui:ydl031w] [pn:similarity to ma helicases] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG405	25430337_f3_2	5528	19631	810	270	YDL031W	776	3.5(10)-77	Saccharomyces cerevisiae	[ui:ydl031w] [pn:similarity to ma helicases] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
b2x12979.x	5331552_fl_1	5529	19632	561	187	YDL031W	400	3.2(10)-36	Saccharomyces cerevisiae	[ui:ydl031w] [pn:similarity to ma helicases] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG571	3947692_fl_1	5530	19633	411	137	YDR043C	233	1.2(10)-19	Saccharomyces cerevisiae	[ui:ydr043c] [pn:weak similarity to k.marxianus mig1 and other regulatory proteins] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5754	23550337_c1_24	5531	19634	900	300	YDR429C	479	1.0(10)-45	Saccharomyces cerevisiae	[ui:ydr429c] [pn:similarity to nuclear ma binding proteins] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4050	1204390_c3_6	5532	19635	1002	334	YGL171W	453	5.9(10)-43	Saccharomyces cerevisiae	[ui:ygl171w] [pn:atp-dependent ma helicase:atp-dependent ma helicase rok1] [gn:rok1:g1651] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
b1x13309.x	3020816_fl_1	5533	19636	609	203	YGL171W	706	9.1(10)-70	Saccharomyces cerevisiae	[ui:ygl171w] [pn:atp-dependent ma helicase:atp-dependent ma helicase rok1] [gn:rok1:g1651] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2561	34179687_c3_3	5534	19637	510	170	YGL127C	185	1.5(10)-14	Saccharomyces cerevisiae	[ui:yg127c] [pn:allows hpr1 null mutant to grow at 37 deg:soh1 protein] [gn:soh1:g2864] [gtcf:10.2:10.8] [keggfc:14.2] [sgdfc:3.7.0:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2747	2151131_c2_3	5535	19638	1170	390	YGL014W	356	6.2(10)-49	Saccharomyces cerevisiae	[ui:yg014w] [pn:similarity to drosophila pumilio protein and mpt5p protein:hypothetical regulatory protein in pdr6-pdr1 intergenic region] [gn:yg1023] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5525	4329575_fl_3	5536	19639	1749	583	YGL014W	476	1.6(10)-44	Saccharomyces cerevisiae	[ui:yg014w] [pn:similarity to drosophila pumilio protein and mpt5p protein:hypothetical regulatory protein in pdr6-pdr1 intergenic region] [gn:yg1023] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3729	16829030_cl_4	5537	19640	1311	437	YGR067C	231	4.5(10)-17	Saccharomyces cerevisiae	[ui:ygr067c] [pn:weak similarity to transcription factors:putative 91.0 kd zinc finger protein in spt4-rom1 intergenic region] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2764	22055252_c2_11	5538	19641	1104	368	YHR169W	1072	1.5(10)-108	Saccharomyces cerevisiae	[ui:yhr169w] [pn:strong similarity to dead box ma helicases:putative atp-dependent ma helicase yhr169w] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5584	15017211_c3_13	5539	19642	228	76	YHR169W	181	2.2(10)-13	Saccharomyces cerevisiae	[ui:yhr169w] [pn:strong similarity to dead box rna helicases;putative atp-dependent rna helicase yhr169w] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3603	34179556_c2_6	5540	19643	1665	555	YHR170W	1516	1.3(10)-155	Saccharomyces cerevisiae	[ui:yhr170w] [pn:nonsense-mediated mma decay protein:nonsense-mediated mma decay protein 3] [gn:nmd3] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5333	30719437_f2_2	5541	19644	480	160	YHR170W	141	6.7(10)-9	Saccharomyces cerevisiae	[ui:yhr170w] [pn:nonsense-mediated mma decay protein:nonsense-mediated mma decay protein 3] [gn:nmd3] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5757	21509380_f2_3	5542	19645	2139	713	YIL105C	507	1.1(10)-48	Saccharomyces cerevisiae	[ui:yil105c] [pn:weak similarity to probable transcription factor ask10p:hypothetical 78.0 kd protein in pfk26-sga1 intergenic region] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5722	1375400_f2_7	5543	19646	3651	1217	YIL030C	577	1.1(10)-86	Saccharomyces cerevisiae	[ui:yil030c] [pn:involved in mma turnover:ssm4 protein] [gn:ssm4:yi3299] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3532	26369157_c2_10	5544	19647	771	257	YIR001C	216	7.7(10)-18	Saccharomyces cerevisiae	[ui:yir001c] [pn:similarity to d.melanogaster ma binding protein:hypothetical 29.0 kd protein in bet1-pan1 intergenic region] [gn:yib1c] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3773	26370316_f2_3	5545	19648	513	171	YIR001C	238	3.6(10)-20	Saccharomyces cerevisiae	[ui:yir001c] [pn:similarity to d.melanogaster ma binding protein:hypothetical 29.0 kd protein in bet1-pan1 intergenic region] [gn:yib1c] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5223	3917563_c3_14	5546	19649	1071	357	YIR005W	255	5.7(10)-22	Saccharomyces cerevisiae	[ui:yir005w] [pn:similarity to ma-binding proteins:hypothetical 17.1 kd protein in bet1-pan1 intergenic region] [gn:yib5w] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5594	31298426_c1_12	5547	19650	297	99	YIL124C	134	3.7(10)-9	Saccharomyces cerevisiae	[ui:yil124c] [pn:weak similarity to human sm protein g:hypothetical 20.3 kd protein in gcd14-pos18 intergenic region] [gn:j0714] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4617	15626338_f2_2	5548	19651	2289	763	YML017W	156	3.0(10)-11	Saccharomyces cerevisiae	[ui:yml017w] [pn:suppressor of dna polymerase alpha mutation:psp2 protein] [gn:psp2:ym9571] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5315	24300255_f2_4	5549	19652	873	291	YMR213W	359	1.7(10)-32	Saccharomyces cerevisiae	[ui:ymr213w] [pn:similarity to s.pombe putative transcription factor cdc5:hypothetical 67.7 kd protein in rar1-scj1 intergenic region] [gn:ym9646] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1236	15761316_c2_5	5550	19653	531	177	YNL255C	398	4.0(10)-37	Saccharomyces cerevisiae	[ui:ynl255c] [pn:strong similarity to nucleic acid-binding proteins:hypothetical 17.1 kd protein in sip3-mrp130 intergenic region] [gn:n0852] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5079	6054138_c2_8	5551	19654	1233	411	YNL175C	583	9.9(10)-57	Saccharomyces cerevisiae	[ui:ynl175c] [pn:similarity to s.pombe rnp24p:hypothetical 45.7 kd protein in rps3-psd1 intergenic region] [gn:n1665] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4233	23489151_c3_4	5552	19655	330	110	YNL027W	259	2.1(10)-21	Saccharomyces cerevisiae	[ui:ynl027w] [pn:similarity to zinc-finger proteins:hypothetical 76.3 kd zinc finger protein in hhf2-ume3 intergenic region] [gn:n2760] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4828	2150313_c1_7	5553	19656	1245	415	YNL027W	188	8.0(10)-12	Saccharomyces cerevisiae	[ui:ynl027w] [pn:similarity to zinc-finger proteins:hypothetical 76.3 kd zinc finger protein in hhf2-ume3 intergenic region] [gn:n2760] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5723	4119002_c3_35	5554	19657	288	96	YNR063W	135	3.7(10)-8	Saccharomyces cerevisiae	[ui:ynr063w] [pn:weak similarity to cyc1/cyp3 transcription activator:putative transcriptional regulatory protein in bio3-hxt17 intergenic region] [gn:n3531] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5781	16831535_c3_32	5555	19658	1632	544	YOR244W	1180	7.0(10)-132	Saccharomyces cerevisiae	[ui:yor244w] [pn:similarity to sas2p and sas3p] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3139	9773376_c3_12	5556	19659	795	265	YPL230W	271	1.1(10)-23	Saccharomyces cerevisiae	[ui:ypl230w] [pn:similarity to transcription factors] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2137	13759635_f2_1	5557	19660	402	134	YPL133C	138	1.1(10)-8	Saccharomyces cerevisiae	[ui:ypl133c] [pn:weak similarity to transcription factors:putative transcriptional regulatory protein in mkk2-cox11 intergenic region] [gn:ipi12c] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2962	9852266_f3_3	5558	19661	1185	395	YPL133C	873	6.2(10)-97	Saccharomyces cerevisiae	[ui:ypl133c] [pn:weak similarity to transcription factors:putative transcriptional regulatory protein in mkk2-cox11 intergenic region] [gn:ipi12c] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3967	47885_f2_2	5559	19662	1143	381	YPR013C	187	2.2(10)-13	Saccharomyces cerevisiae	[ui:ypr013c] [pn:similarity to transcription factors] [gtcf:10.2] [keggf:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2677	34663912_c2_8	5560	19663	2001	667	YPR031W	833	2.7(10)-92	Saccharomyces cerevisiae	[ui:ypr031w] [pn:similarity to human zinc-finger protein brl40] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2941	4569427_f1_1	5561	19664	774	258	YPR031W	117	0.00038	Saccharomyces cerevisiae	[ui:ypr031w] [pn:similarity to human zinc-finger protein brl40] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5797	4476387_c3_36	5562	19665	657	219	YPR107C	655	2.2(10)-64	Saccharomyces cerevisiae	[ui:ypr107c] [pn:strong similarity to d.melanogaster zinc finger protein] [gtcf:10.2] [keggfc:14.2] [sgdfc:4.12.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4909	7827_f1_1	5563	19666	1620	540	YHR065C	1309	1.2(10)-133	Saccharomyces cerevisiae	[ui:yhr065c] [pn:required for maturation of the 35s primary transcript:atp-dependent rna helicase] [gn:rrp3] [gtcf:10.3] [keggfc:14.2] [sgdfc:4.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3377	2737785_c2_7	5564	19667	648	216	YJL033W	214	1.8(10)-16	Saccharomyces cerevisiae	[ui:yjl033w] [pn:can suppress the u14 snorna rna processing function:probable atp-dependent ma helicase ca4] [gn:hca4:j1250] [gtcf:10.3] [keggfc:14.2] [sgdfc:4.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5717	1253_f2_1	5565	19668	2430	810	YJL033W	1949	1.8(10)-201	Saccharomyces cerevisiae	[ui:yjl033w] [pn:can suppress the u14 snorna rna processing function:probable atp-dependent ma helicase ca4] [gn:hca4:j1250] [gtcf:10.3] [keggfc:14.2] [sgdfc:4.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5118	1213187_fl_2	5566	19669	564	188	YLR059C	353	2.2(10)-32	Saccharomyces cerevisiae	[ui:ylr059c] [pn:suppressor of rna 12/yme2:ynt20 protein] [gn:ynt20:12159] [gtcf:10.3] [keggf:14.2] [sgdfc:4.2.0] [db:gtc-saccharomyces cerevisiae]
b2x13585.y	6561_c3_2	5567	19670	297	99	YBL092W	377	6.7(10)-35	Saccharomyces cerevisiae	[ui:ybl092w] [pn:ribosomal protein l32.e:60s ribosomal protein l32e] [gn:ybl0838] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5763	12501050_c2_21	5568	19671	372	124	YBL087C	583	9.9(10)-57	Saccharomyces cerevisiae	[ui:ybl087c] [pn:ribosomal protein l23.e:60s ribosomal protein l17] [gn:rp117b:rp117a:ybl0713] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5062	36367178_f3_4	5569	19672	627	209	YBL072C	697	8.1(10)-69	Saccharomyces cerevisiae	[ui:ybl072c] [pn:ribosomal protein s8.e:40s ribosomal protein s8:s14:ys9:rp19] [gn:rrp8b:rrp8a:ybl0613:ybl06] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG44	24492149_c1_2	5570	19673	336	112	YBL027W	237	4.5(10)-20	Saccharomyces cerevisiae	[ui:ybl027w] [pn:ribosomal protein l19.e:60s ribosomal protein l19:l23:y114:rp33:rp15l] [gn:rp119a:ybr084bc:rp119b:ybr084c-a:ybl0424] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5370	9773444_c1_8	5571	19674	414	138	YBL027W	206	8.8(10)-17	Saccharomyces cerevisiae	[ui:ybl027w] [pn:ribosomal protein 119.e:60s ribosomal protein 119.i23.y114:rp33:rp15l] [gn:rp119a:ybr084bc:rp119b:ybr084c-a:ybl0424] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4531	22542162_c2_12	5572	19675	207	69	YBR031W	297	2.0(10)-26	Saccharomyces cerevisiae	[ui:ybr031w] [pn:ribosomal protein 12a:60s ribosomal protein 12a:rp2] [gn:rp12a:rp12:ybr0315] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4531	10984406_c2_11	5573	19676	252	84	YBR031W	143	2.1(10)-9	Saccharomyces cerevisiae	[ui:ybr031w] [pn:ribosomal protein 12a:60s ribosomal protein 12a:rp2] [gn:rp12a:rp12:ybr0315] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
b9x13909.x	14188817_fl_1	5574	19677	603	201	YBR031W	619	1.5(10)-60	Saccharomyces cerevisiae	[ui:ybr031w] [pn:ribosomal protein 12a:60s ribosomal protein 12a:rp2] [gn:rp12a:rp12:ybr0315] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4334	4475811_f3_4	5575	19678	423	141	YBR048W	574	8.9(10)-56	Saccharomyces cerevisiae	[ui:ybr048w] [pn:ribosomal protein s11.e.b:ribosomal protein s11.e:40s ribosomal protein rp41:ys12:s18a/s18b] [gn:tps18b:ybr0501:tps18a:yd9813] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2123	10192175_f1_1	5576	19679	363	121	YBR181C	475	2.7(10)-45	Saccharomyces cerevisiae	[ui:ybr181c] [pn:ribosomal protein s6.e:40s ribosomal protein s6.s10:ys4:rp9] [gn:rps10a:rps6a:rps10l:ybr1244] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2123	21901556_f3_7	5577	19680	204	68	YBR181C	164	2.5(10)-12	Saccharomyces cerevisiae	[ui:ybr181c] [pn:ribosomal protein s6.e:40s ribosomal protein s6.s10:ys4:rp9] [gn:rps10a:rps6a:rps10l:ybr1244] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5383	19578141_c3_15	5578	19681	618	206	YBR189W	787	2.3(10)-78	Saccharomyces cerevisiae	[ui:ybr189w] [pn:ribosomal protein s9.e:b:40s ribosomal protein ys11:yp28:s13] [gn:rps13a:ys11a:rps13b:sup46:ybr1317] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2827	29511007_c1_4	5579	19682	216	72	YBR191W	220	2.8(10)-18	Saccharomyces cerevisiae	[ui:ybr191w] [pn:ribosomal protein l21.e:60s ribosomal protein l21e] [gn:urp1a:urp1:ybr1401] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5383	33359385_c1_7	5580	19683	201	67	YBR191W	205	1.1(10)-16	Saccharomyces cerevisiae	[ui:ybr191w] [pn:ribosomal protein l21.e:60s ribosomal protein l21e] [gn:urp1a:urp1:ybr1401] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5163	24414078_fl_1	5581	19684	900	300	YDL202W	466	2.5(10)-44	Saccharomyces cerevisiae	[ui:ydl202w] [pn:weak similarity to ribosomal protein] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5492	23486658_fl_2	5582	19685	360	120	YDL191W	376	8.5(10)-35	Saccharomyces cerevisiae	[ui:ydl191w] [pn:ribosomal protein:60s ribosomal protein l35e] [gn:sosl:d1249:sos2:d2170] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5216	23718757_fl_6	5583	19686	408	136	YDL083C	529	5.2(10)-51	Saccharomyces cerevisiae	[ui:ydl083c] [pn:ribosomal protein sl6.e:40s ribosomal protein rs16 homolog:rp61r homolog] [gn:rps16b:rps16a:rp61r:ym9375] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5216	9770037_c2_13	5584	19687	669	223	YDL082W	658	1.1(10)-64	Saccharomyces cerevisiae	[ui:ydl082w] [pn:ribosomal protein l13] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1465	12922192_fl_1	5585	19688	402	134	YDL081C	204	1.3(10)-16	Saccharomyces cerevisiae	[ui:ydl081c] [pn:acidic ribosomal protein al:60s acidic ribosomal protein p1-alpha:a1:l12eia] [gn:rplal:l12eii:rpal] [gtcf:10.4:10.7] [keggf:14.2] [sgdfc:5.1.0:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5216	13703275_f1_3	5586	19689	333	111	YDL081C	262	1.0(10)-22	Saccharomyces cerevisiae	[ui:ydl081c] [pn:acidic ribosomal protein p1-alpha:a1:112e1a] [gn:rpl112e1a:rpl1] [gtcf:10.4:10.7] [keggf:14.2] [sgdfc:5.1.0:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
b2x14827.y	6145175_f3_2	5587	19690	201	67	YDL075W	206	8.8(10)-17	Saccharomyces cerevisiae	[ui:ydl075w] [pn:ribosomal protein l31.e:60s ribosomal protein l34.y128] [gn:rp134:rp134a:rp134b:l8084] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4967	36615676_f3_6	5588	19691	447	149	YDR041W	184	1.8(10)-14	Saccharomyces cerevisiae	[ui:ydr041w] [pn:weak similarity to bacterial ribosomal s10 proteins] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4935	4195268_f3_2	5589	19692	435	145	YDR064W	685	1.5(10)-67	Saccharomyces cerevisiae	[ui:ydr064w] [pn:ribosomal protein:40s ribosomal protein s13:ys15:s27a] [gn:ys15:tps13:ydr9609] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5053	21604035_c2_11	5590	19693	405	135	YDR115W	197	7.9(10)-16	Saccharomyces cerevisiae	[ui:ydr115w] [pn:similarity to bacterial ribosomal l34 proteins] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3607	25800716_c3_8	5591	19694	444	148	YDR116C	239	2.7(10)-20	Saccharomyces cerevisiae	[ui:ydr116c] [pn:similarity to bacterial ribosomal 11 proteins] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
b3x13209.x	23548178_f3_1	5592	19695	261	87	YDR237W	196	1.0(10)-15	Saccharomyces cerevisiae	[ui:ydr237w] [pn:similarity to bacterial ribosomal 15 protein:mitochondrial 60s ribosomal protein 17 precursor:ym17] [gn:mrpl7:yd8419] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4623	16286629_c1_5	5593	19696	615	205	YDR237W	459	1.3(10)-43	Saccharomyces cerevisiae	[ui:ydr237w] [pn:similarity to bacterial ribosomal 15 protein:mitochondrial 60s ribosomal protein 17 precursor:ym17] [gn:mrpl7:yd8419] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4056	19690675_c1_4	5594	19697	369	123	YDR382W	245	6.5(10)-21	Saccharomyces cerevisiae	[ui:ydr382w] [pn:acidic ribosomal protein:60s acidic ribosomal protein p2-beta:145.y144c:ypa1:112eia] [gn:rpla4:112eia:rp145] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0-9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3711	6031261_c1_7	5595	19698	354	118	YDR382W	188	7.0(10)-15	Saccharomyces cerevisiae	[ui:ydr382w] [pn:acidic ribosomal protein:60s acidic ribosomal protein p2-beta:145.y144c:ypa1:112eia] [gn:rpla4:112eia:rp145] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0-9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5811	12932805_f2_13	5596	19699	504	168	YDR418W	739	2.8(10)-73	Saccharomyces cerevisiae	[ui:ydr418w] [pn:ribosomal protein 112.e:60s ribosomal protein 112.y115.y123] [gn:rp115b:rp115a:d9461] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5562	1031517_c3_15	5597	19700	408	136	YDR450W	540	3.6(10)-52	Saccharomyces cerevisiae	[ui:ydr450w] [pn:ribosomal protein s18.e:c4:ribosomal protein s18.e:c13:40s ribosomal protein s18e] [gn:rps18b:rps18a:rps13c:ydr064w:d9461] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2546	6831302_f2_2	5598	19701	342	114	YDR500C	365	1.2(10)-33	Saccharomyces cerevisiae	[ui:ydr500c] [pn:ribosomal protein 1.37.e:60s ribosomal protein 137e b:yp55] [gn:rp135b:d9719] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3339	26210927_c3_8	5599	19702	402	134	YDR500C	357	8.8(10)-33	Saccharomyces cerevisiae	[ui:ydr500c] [pn:ribosomal protein 1.37.e:60s ribosomal protein 137e b:yp55] [gn:rp135b:d9719] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5720	26353216_c3_29	5600	19703	828	276	YEL050C	733	1.3(10)-72	Saccharomyces cerevisiae	[ui:yel050c] [pn:similarity to bacterial ribosomal 12 protein:putative 60s ribosomal protein yel050c] [gn:sygp-orf37] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5720	26370418_c2_22	5601	19704	549	183	YEL050C	199	1.8(10)-15	Saccharomyces cerevisiae	[ui:yel050c] [pn:similarity to bacterial ribosomal l2 protein:putative 60s ribosomal protein yel050c] [gn:sygp-orf37] [gicfc:10.4] [keggfc:14.2] [sgdgc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3279	2189062_fl_1	5602	19705	465	155	YER074W	498	1.0(10)-47	Saccharomyces cerevisiae	[ui:yer074w] [pn:ribosomal protein s24.e:40s ribosomal protein s24.e:rp50] [gn:rp50a:rp50b:rp524ea:rp524eb] [gicfc:10.4] [keggfc:14.2] [sgdgc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5435	12926550_c2_14	5603	19706	366	122	YGL189C	522	2.8(10)-50	Saccharomyces cerevisiae	[ui:ygl189c] [pn:40s ribosomal protein s26c.c7:40s ribosomal protein s26e-a] [gn:rp526a:rp526:g1355] [gicfc:10.4] [keggfc:14.2] [sgdgc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4954	10979677_c2_14	5604	19707	660	220	YGL135W	897	5.2(10)-90	Saccharomyces cerevisiae	[ui:ygl135w] [pn:ribosomal protein:60s ribosomal protein l10a] [gn:ssm1b:ssm2:g2834:ssm1a:yp122 0w:ssm1] [gicfc:10.4] [keggfc:14.2] [sgdgc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5409	10975925_f2_7	5605	19708	756	252	YGL123W	836	1.5(10)-83	Saccharomyces cerevisiae	[ui:ygl123w] [pn:ribosomal protein:40s ribosomal protein s4:omnipotent suppressor protein sup44:rp12:s2e] [gn:sup44:g2893] [gicfc:10.4] [keggfc:14.2] [sgdgc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2928	26364033_c1_6	5606	19709	627	209	YGL076C	850	5.0(10)-85	Saccharomyces cerevisiae	[ui:ygl076c] [pn:ribosomal protein y18:16:rp11] [gn:rp16a:rp16:rp18a:y18a] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4731	5275312_f2_5	5607	19710	471	157	YGL031C	475	2.7(10)-45	Saccharomyces cerevisiae	[ui:ygl031c] [pn:ribosomal protein l24.e.a:60s ribosomal protein l30a:rp29:y121] [gn:rp130a:rp29] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3829	30178908_c3_7	5608	19711	318	106	YGL030W	410	2.1(10)-38	Saccharomyces cerevisiae	[ui:ygl030w] [pn:ribosomal protein l30.e:60s ribosomal protein l30e:y132:rp73] [gn:rp132] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG545	10445193_c2_4	5609	19712	219	73	YGR027C	255	5.7(10)-22	Saccharomyces cerevisiae	[ui:ygr027c] [pn:ribosomal protein s25.e.c7] [gn:rps31a] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5036	10739130_c1_8	5610	19713	522	174	YGR085C	789	1.5(10)-78	Saccharomyces cerevisiae	[ui:ygr085c] [pn:ribosomal protein y116.b:60s ribosomal protein l16:y116:39a:rp39] [gn:rp116b:rp39b] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5247	35392568_c2_15	5611	19714	576	192	YGR118W	723	1.3(10)-71	Saccharomyces cerevisiae	[ui:ygr118w] [pn:ribosomal protein s23 e:40s ribosomal protein s28] [gn:rs28a:rs28b:p9659] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
b1x14649.x	11177068_fl_1	5612	19715	660	220	YGR214W	715	1.0(10)-70	Saccharomyces cerevisiae	[ui:ygr214w] [pn:40s ribosomal protein p40 homolog a:40s ribosomal protein sa homolog a:nucleic acid-binding protein nab1a] [gn:nab1a:nab1:yst1] [gtcf:10.4:12.16] [keggfc:14.2] [sgdfc:5.1.0:6.4.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5577	4820187_fl_2	5613	19716	231	77	YHL015W	243	1.1(10)-20	Saccharomyces cerevisiae	[ui:yhl015w] [pn:ribosomal protein:40s ribosomal protein] [gn:urp2] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5735	1564051_c2_17	5614	19717	393	131	YHR010W	458	1.7(10)-43	Saccharomyces cerevisiae	[ui:yhr010w] [pn:ribosomal protein 127 e:probable 60s ribosomal protein 127] [gn:rp127a:rp127b:yrp471w:d8035] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5339	23441910_f2_4	5615	19718	582	194	YHR148W	763	8.3(10)-76	Saccharomyces cerevisiae	[ui:yhr148w] [pn:similarity to ribosomal protein:putative 40s ribosomal protein yhr148w] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5795	428_f3_20	5616	19719	708	236	YIL133C	766	4.0(10)-76	Saccharomyces cerevisiae	[ui:yil133c] [pn:ribosomal protein:60s ribosomal protein l13a:rp22] [gn:rp22:rp113a] [gtcf:10.4] [keggf:14.2] [sgdf:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3584	23546950_f2_2	5617	19720	789	263	YIL018W	1116	3.2(10)-113	Saccharomyces cerevisiae	[ui:yil018w] [pn:ribosomal protein l8.e:60s ribosomal protein y16:l5:rp8] [gn:rp15b:yfr031bc:rp15a] [gtcf:10.4] [keggf:14.2] [sgdf:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1243	4680_f2_1	5618	19721	327	109	YIL190C	434	6.0(10)-41	Saccharomyces cerevisiae	[ui:yil190c] [pn:ribosomal protein s15a.e.c10:40s ribosomal protein s22:ys24:yp58] [gn:rps24a:rps24:j0355:rps24b:l8039] [gtcf:10.4] [keggf:14.2] [sgdf:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG975	14882762_c2_3	5619	19722	186	62	YIL190C	208	5.4(10)-17	Saccharomyces cerevisiae	[ui:yil190c] [pn:ribosomal protein s15a.e.c10:40s ribosomal protein s22:ys24:yp58] [gn:rps24a:rps24:j0355:rps24b:l8039] [gtcf:10.4] [keggf:14.2] [sgdf:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5151	23837563_f2_2	5620	19723	354	118	YIL177W	359	5.4(10)-33	Saccharomyces cerevisiae	[ui:yil177w] [pn:ribosomal protein l17.e:60s ribosomal protein y117-b] [gn:rp120b:j0493] [gtcf:10.4] [keggf:14.2] [sgdf:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3372	34433128_f3_5	5621	19724	210	70	YJL177W	129	1.3(10)-8	Saccharomyces cerevisiae	[ui:yjl177w] [pn:ribosomal protein l17.e:60s ribosomal protein yjl17-b] [gn:rp120b;j0493] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5328	20320378_c2_15	5622	19725	195	65	YJL136C	258	2.7(10)-22	Saccharomyces cerevisiae	[ui:yjl136c] [pn:ribosomal protein s21.e] [gn:rps25b] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4189	10979656_c2_4	5623	19726	684	228	YJR123W	873	1.8(10)-87	Saccharomyces cerevisiae	[ui:yjr123w] [pn:ribosomal protein s5.e:40s ribosomal protein s5:rp14:ys8] [gn:rps5;j2045] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3175	32282527_c2_5	5624	19727	321	107	YJR145C	251	1.5(10)-21	Saccharomyces cerevisiae	[ui:yjr145c] [pn:ribosomal protein s4.e:c10:40s ribosomal protein s4:s7:ys6:rp5] [gn:rps7b;j2186] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5815	36366532_f2_15	5625	19728	795	265	YJR145C	1118	2.0(10)-113	Saccharomyces cerevisiae	[ui:yjr145c] [pn:ribosomal protein s4.e:c10:40s ribosomal protein s4:s7:ys6:rp5] [gn:rps7b;j2186] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4699	2117752_c3_9	5626	19729	357	119	YKL156W	316	1.8(10)-28	Saccharomyces cerevisiae	[ui:ykl156w] [pn:ribosomal protein s27.e:40s ribosomal protein s27-1] [gn:rps27a] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0.9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5791	33306557_c2_24	5627	19730	696	232	YKL009W	862	2.7(10)-86	Saccharomyces cerevisiae	[ui:ykl009w] [pn:weak similarity to red goosefoot acidic ribosomal protein p0 and m.jannaschii acidic ribosomal protein p0:hypothetical 27.1 kd protein ufd4-cap l intergenic region] [gn:ykl160] [gtcf:10.4] [keggf:14.2] [sgdf:5.1.0]
CONTIG3549	25431253_c2_5	5628	19731	285	95	YKL006W	255	5.7(10)-22	Saccharomyces cerevisiae	[ui:ykl006w] [pn:ribosomal protein:probable 60s ribosomal protein l14ea] [gn:rpl14a:ykl153] [gtcf:10.4] [keggf:14.2] [sgdf:5.1.0;9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3386	4081505_c1_3	5629	19732	609	203	YLL045C	840	5.7(10)-84	Saccharomyces cerevisiae	[ui:yll045c] [pn:ribosomal protein 17a.e.b:60s ribosomal protein 17a-1:14-1:y15:rp6] [gn:rpl4b] [gtcf:10.4] [keggf:14.2] [sgdf:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4586	4770001_c3_7	5630	19733	798	266	YLL045C	993	3.5(10)-100	Saccharomyces cerevisiae	[ui:yll045c] [pn:ribosomal protein 17a.e.b:60s ribosomal protein 17a-1:14-1:y15:rp6] [gn:rpl4b] [gtcf:10.4] [keggf:14.2] [sgdf:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2752	20423136_f1_1	5631	19734	612	204	YLR009W	544	1.3(10)-52	Saccharomyces cerevisiae	[ui:ylr009w] [pn:similarity to ribosomal protein l24.e.b] [gtcf:10.4] [keggf:14.2] [sgdf:5.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5362	24797507_c2_15	5632	19735	363	121	YLR061W	231	2.0(10)-19	Saccharomyces cerevisiae	[ui:ylr061w] [pn:ribosomal protein:60s ribosomal protein y131] [gn:12168] [gtcf:10.4] [keggf:14.2] [sgdf:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1362	1363817_f3_2	5633	19736	198	66	YLR075W	233	1.2(10)-19	Saccharomyces cerevisiae	[ui:ylr075w] [pn:ribosomal protein:ubiquinol-cytochrome c reductase complex subunit vi requiring protein] [gn:qsr1:grc5] [gtcf:10.4:12.8] [keggf:14.2] [sgdf:3.8.0:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4663	4453427_f2_2	5634	19737	753	251	YLR075W	916	5.0(10)-92	Saccharomyces cerevisiae	[ui:ylr075w] [pn:ribosomal protein:ubiquinol-cytochrome c reductase complex subunit vi requiring protein] [gn:qsr1:grc5] [gtcf:10.4:12.8] [keggf:14.2] [sgdf:3.8.0:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3605	21539018_f3_3	5635	19738	189	63	YLR287C-A	189	5.5(10)-15	Saccharomyces cerevisiae	[ui:ylr287c-a] [pn:ribosomal protein:strong similarity to human ubiquitin-like protein/ribosomal protein s30] [gn:rps30a:rps30b] [gtcf:10.4] [keggf:14.2] [sgdf:5.1.0] [db:gtc-saccharomyces cerevisiae]
b3x14645.x	12672056_c3_2	5636	19739	264	88	YLR325C	206	8.8(10)-17	Saccharomyces cerevisiae	[ui:ylr325c] [pn:putative ribosomal protein l38;putative 60s ribosomal protein l38] [gn:l8543] [gtcf:10.4] [keggf:14.2] [sgdf:5.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4548	29332305_c3_7	5637	19740	315	105	YLR340W	142	1.8(10)-9	Saccharomyces cerevisiae	[ui:ylr340w] [pn:acidic ribosomal protein p0:110e] [gn:rpla0:rp110e:110e:18300] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4875	25835912_f3_5	5638	19741	525	175	YLR340W	594	6.7(10)-58	Saccharomyces cerevisiae	[ui:ylr340w] [pn:acidic ribosomal protein p0:110e] [gn:rpla0:rp110e:110e:18300] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4263	24016512_c1_6	5639	19742	393	131	YLR344W	508	8.8(10)-49	Saccharomyces cerevisiae	[ui:ylr344w] [pn:ribosomal protein:60s ribosomal protein 126-a:y133] [gn:rp133a:rp126a:rp126:18300] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4231	5338452_fl_1	5640	19743	399	133	YML073C	460	1.1(10)-43	Saccharomyces cerevisiae	[ui:ym1073c] [pn:ribosomal protein:60s ribosomal protein] [gn:y116a] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4687	13671937_c2_11	5641	19744	843	281	YML063W	961	8.6(10)-97	Saccharomyces cerevisiae	[ui:ym1063w] [pn:ribosomal protein s3a.e:40s ribosomal protein rp10b] [gn:rp10b:rp10b:plc2] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG2652	13775442_f3_4	5642	19745	615	205	YMR121C	787	2.3(10)-78	Saccharomyces cerevisiae	[ui:ymr121c] [pn:ribosomal protein l15.e.c13:60s ribosomal protein y110 b:113:rp15r:yp18] [gn:rp113b:rp110b:ym8564] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
b1x10611.y	22742890_f2_2	5643	19746	324	108	YMR188C	174	2.2(10)-13	Saccharomyces cerevisiae	[ui:ymr188c] [pn:weak similarity to 30s ribosomal protein s17] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2692	15664802_c2_6	5644	19747	300	100	YMR194W	260	1.7(10)-22	Saccharomyces cerevisiae	[ui:ymr194w] [pn:ribosomal protein:60s ribosomal protein y139] [gn:rp139a:rp139:ym9646] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3837	2928442_c3_9	5645	19748	342	114	YMR230W	292	6.7(10)-26	Saccharomyces cerevisiae	[ui:ymr230w] [pn:strong similarity to ribosomal protein s10:putative 40s ribosomal protein in mtfl-rnh1 intergenic region] [gn:ym9959] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3701	1054677_c2_7	5646	19749	561	187	YMR242C	738	3.7(10)-73	Saccharomyces cerevisiae	[ui:ymr242c] [pn:ribosomal protein:60s ribosomal protein l18a] [gn:rp118a:rp118a:ym9408] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5802	24016500_fl_13	5647	19750	447	149	YNL302C	632	6.4(10)-62	Saccharomyces cerevisiae	[ui:ynl302c] [pn:ribosomal protein s19.e:40s ribosomal protein s19b.s16b:ys16:rp55] [gn:rp55b:tps16b:n0422] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3291	5132933_c3_9	5648	19751	495	165	YNL301C	571	1.8(10)-55	Saccharomyces cerevisiae	[ui:ynl301c] [pn:ribosomal protein l18.e:ribosomal protein s18.e:60s ribosomal protein l18:rp28] [gn:rp28b:rp28a:n0425] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5406	2189382_c3_12	5649	19752	864	288	YNL284C	650	7.9(10)-64	Saccharomyces cerevisiae	[ui:ynl284c] [pn:similarity to ribosomal protein l15:mitochondrial 60s ribosomal protein l10 precursor:ynl10] [gn:mrpl10:n0580] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1882	16605383_fl_2	5650	19753	393	131	YNL185C	359	5.4(10)-33	Saccharomyces cerevisiae	[ui:ynl185c] [pn:strong similarity to ribosomal protein l11:putative 60s mitochondrial ribosomal protein ynl185c] [gn:n1623] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3963	35672937_c2_5	5651	19754	192	64	YNL185C	154	2.8(10)-11	Saccharomyces cerevisiae	[ui:ynl185c] [pn:strong similarity to ribosomal protein l11:putative 60s mitochondrial ribosomal protein ynl185c] [gn:n1623] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG617	25565962_f2_2	5652	19755	561	187	YNL178W	568	3.7(10)-55	Saccharomyces cerevisiae	[ui:ynl178w] [pn:ribosomal protein s3.e:40s ribosomal protein s3:ys3:rp13] [gn:rps3:suf14:n1653] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5558	29378811_f3_9	5653	19756	336	112	YNL162W	526	1.1(10)-50	Saccharomyces cerevisiae	[ui:ynl162w] [pn:ribosomal protein l36a.e] [gn:rp141a] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5165	4878516_f2_6	5654	19757	378	126	YNL081C	287	2.2(10)-25	Saccharomyces cerevisiae	[ui:ynl081c] [pn:similarity to ribosomal protein s13:putative 40s mitochondrial ribosomal protein ynl081c] [gn:n2322] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1297	31382010_f1_1	5655	19758	186	62	YNL067W	200	3.7(10)-16	Saccharomyces cerevisiae	[ui:ynl067w] [pn:ribosomal protein l9.e:c14:60s ribosomal protein l9b:yl11:rp25] [gn:rp19b:n2406:ynl2406w] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3671	4954192_c2_3	5656	19759	399	133	YNL002C	156	5.7(10)-11	Saccharomyces cerevisiae	[ui:ynl002c] [pn:ribosomal protein l7.e:60s ribosomal protein l7] [gn:rp17:rp7:n2014] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5057	24428437_f2_2	5657	19760	381	127	YNL002C	146	7.5(10)-10	Saccharomyces cerevisiae	[ui:ynl002c] [pn:ribosomal protein l7.e:60s ribosomal protein l7] [gn:rlp7:rlp7:n201.4] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1854	12610930_f1_1	5658	19761	591	197	YNR036C	423	8.9(10)-40	Saccharomyces cerevisiae	[ui:ynr036c] [pn:strong similarity to ribosomal protein s12:putative 40s mitochondrial ribosomal protein ynr036c] [gn:n3298] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG653	12610930_f3_2	5659	19762	597	199	YNR036C	420	1.8(10)-39	Saccharomyces cerevisiae	[ui:ynr036c] [pn:strong similarity to ribosomal protein s12:putative 40s mitochondrial ribosomal protein ynr036c] [gn:n3298] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5496	1953127_c2_16	5660	19763	438	146	YOL127W	527	8.5(10)-51	Saccharomyces cerevisiae	[ui:yol127w] [pn:ribosomal protein l23a.c:60s ribosomal protein l25.y125:rp611] [gn:rlp125] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4890	24804625_c3_9	5661	19764	387	129	YOL040C	339	7.0(10)-31	Saccharomyces cerevisiae	[ui:yol040c] [pn:ribosomal protein:40s ribosomal protein s15:ys21:rp52:rig protein] [gn:rps15:rps21] [gtcf:10.4] [keggf:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3180	1408438_c2_9	5662	19765	426	142	YOR063W	466	2.5(10)-44	Saccharomyces cerevisiae	[ui:yor063w] [pn:ribosomal protein l3.e:60s ribosomal protein l3:trichodermin resistance protein:yl1:rp1] [gn:tcml:mak8] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
b1x11845.x	10167087_c2_1	5663	19766	801	267	YOR096W	666	1.6(10)-65	Saccharomyces cerevisiae	[ui:yor096w] [pn:ribosomal protein:40s ribosomal protein rp30] [gn:rp30:yor3177w:rps30] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5608	4882938_c1_18	5664	19767	471	157	YOR369C	453	5.9(10)-43	Saccharomyces cerevisiae	[ui:yor369c] [pn:acidic ribosomal protein s12:40s ribosomal protein s12] [gn:rs12:rps12] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5797	3906261_c3_33	5665	19768	318	106	YPL143W	445	4.2(10)-42	Saccharomyces cerevisiae	[ui:yp143w] [pn:ribosomal protein l35a.e.c16:60s ribosomal protein l37a:yl37:rp47] [gn:rp137a:lp14w:p2625] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5634	9791087_c3_29	5666	19769	408	136	YPL131W	331	5.0(10)-30	Saccharomyces cerevisiae	[ui:yp131w] [pn:ribosomal protein l5.e:60s ribosomal protein l1:15:yl3:ribosomal 5 s mia-binding protein] [gn:rp11:lp14w] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5634	12110026_c2_25	5667	19770	636	212	YPL131W	630	1.0(10)-61	Saccharomyces cerevisiae	[ui:ypl131w] [pn:ribosomal protein l5.e:60s ribosomal protein l1:l5.yl3:ribosomal 5 s ma-binding protein] [gn:rp1:l:ip114w] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3400	31501_f3_4	5668	19771	300	100	YPR043W	259	2.1(10)-22	Saccharomyces cerevisiae	[ui:ypr043w] [pn:ribosomal protein l37a.e:probable 60s ribosomal protein l37a] [gn:yp9499] [gtcf:10.4] [keggfc:14.2] [sgdfc:5.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3918	24432842_c3_6	5669	19772	870	290	YDL143W	881	2.6(10)-88	Saccharomyces cerevisiae	[ui:ydl143w] [pn:component of chaperonin-containing t-complex:t-complex protein 1, delta subunit:tcp-1-delta:cct-delta] [gn:cct4:tcp4:anc2] [gtcf:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
b9x11364.y	24665678_c3_2	5670	19773	555	185	YDL143W	705	1.2(10)-69	Saccharomyces cerevisiae	[ui:ydl143w] [pn:component of chaperonin-containing t-complex:t-complex protein 1, delta subunit:tcp-1-delta:cct-delta] [gn:cct4:tcp4:anc2] [gtcf:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4653	1179503_c3_10	5671	19774	246	82	YDR155C	227	5.2(10)-19	Saccharomyces cerevisiae	[ui:ydr155c] [pn:peptidylprolyl isomerase:peptidyl-prolyl cis-trans isomerase:ppiase:rotamase:cyclophi lin:cyclosporin a-binding protein:cph:ppi-ii] [gn:cpr1:cyp1:cph1:sec1:yd8358] [gtcf:10.5:10.7:12.7:13.2:14.1] [ec:5.2.1.8] [keggfc:
CONTIG5279	35781556_c1_11	5672	19775	207	69	YDR155C	236	5.7(10)-20	Saccharomyces cerevisiae	[ui:ydr155c] [pn:peptidylprolyl isomerase:peptidyl-prolyl cis-trans isomerase:ppiase:rotamase:cyclophi lin:cyclosporin a-binding protein:cph:ppi-ii] [gn:cpr1:cyp1:cph1:sec1:yd8358] [gtcf:10.5:10.7:12.7:13.2:14.1] [ec:5.2.1.8] [keggfc:
CONTIG626	10761050_c2_4	5673	19776	1185	395	YDR188W	1303	5.0(10)-133	Saccharomyces cerevisiae	[ui:ydr188w] [pn:component of chaperonin-containing t-complex:zeta subunit:t-complex protein 1, zeta subunit:tcp-1-zeta:cct-zeta] [gn:cct6:tcp6:tcp20:yd9395] [gtcf:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0:9.2.0] [db:gtc-saccharomyc
CONTIG5630	4798262_f3_9	5674	19777	1677	559	YDR212W	2163	3.7(10)-224	Saccharomyces cerevisiae	[ui:ydr212w] [pn:component of chaperonin-containing t-complex:t-complex protein 1, alpha subunit:tcp-1-alpha:cct-alpha] [gn:cct1:tcp1:yd8142] [gtcf:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4322	78192_c3_5	5675	19778	867	289	YDR304C	455	3.6(10)-43	Saccharomyces cerevisiae	[ui:ydr304c] [pn:cyclophilin d of the er:peptidyl-prolyl cis-trans isomerase d precursor:ppiase:rotamase:cyclophilin d] [gn:cpr5:cyp5:cypd:d9740] [gtfc:10.5:10.7:12.16:12.7] [ec:5.2.1.8] [keggfc:14.1] [sgdgc:6.1.0:9.4.0] [db:gtc-sacc
CONTIG5744	32711061_c3_32	5676	19779	741	247	YDR304C	504	2.2(10)-48	Saccharomyces cerevisiae	[ui:ydr304c] [pn:cyclophilin d of the er:peptidyl-prolyl cis-trans isomerase d precursor:ppiase:rotamase:cyclophilin d] [gn:cpr5:cyp5:cypd:d9740] [gtfc:10.5:10.7:12.16:12.7] [ec:5.2.1.8] [keggfc:14.1] [sgdgc:6.1.0:9.4.0] [db:gtc-sacc
CONTIG1065	23453438_c2_1	5677	19780	363	121	YDR519W	250	1.8(10)-21	Saccharomyces cerevisiae	[ui:ydr519w] [pn:fk506/rapamycin-binding protein of the er:fk506-13:fkbp-15:peptidyl-prolyl cis-trans isomerase:ppiase] [gn:fpr2:fkbp2:d9719] [gtfc:10.5:10.7:12.16:12.7:13.2] [ec:5.2.1.8] [keggfc:14.1] [
CONTIG2082	4688425_f3_1	5678	19781	927	309	YER048C	154	9.8(10)-9	Saccharomyces cerevisiae	[ui:yer048c] [pn:dnaj homolog:protein] [gn:caj1] [gtfc:10.5:10.7:12.7] [keggfc:14.2] [sgdgc:6.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3227	3932812_f1_1	5679	19782	609	203	YER048C	163	3.2(10)-17	Saccharomyces cerevisiae	[ui:yer048c] [pn:dnaj homolog:protein] [gn:caj1] [gtcf:10.5:10.7:12.7] [keggf:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4756	3320192_c2_13	5680	19783	591	197	YER048C	215	2.8(10)-17	Saccharomyces cerevisiae	[ui:yer048c] [pn:dnaj homolog:protein] [gn:caj1] [gtcf:10.5:10.7:12.7] [keggf:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4472	34259382_c2_4	5681	19784	1017	339	YFR041C	334	2.3(10)-30	Saccharomyces cerevisiae	[ui:yfr041c] [pn:weak similarity to dnaj-like heat shock proteins:hypothetical 34.2 kd protein in sap155-ymr31 intergenic region precursor] [gtcf:12.7] [keggf:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG883	882781_c2_4	5682	19785	870	290	YIL142W	1022	3.0(10)-103	Saccharomyces cerevisiae	[ui:yil142w] [pn:chaparonin of the tcp1 ring complex, cytosolic:tcp1-beta:cct-beta] [gn:cct2:tcp2:bin3] [gtcf:10.5:10.7:12.7] [keggf:14.2] [sgdfc:6.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3227	24417882_f3_2	5683	19786	300	100	YIR004W	164	1.6(10)-11	Saccharomyces cerevisiae	[ui:yir004w] [pn:similarity to caj1p, ydj1p and to dnaj-like proteins:hypothetical 48.6 kd protein in bet1-pan1 intergenic region] [gn:yib4w] [gtcf:10.5:10.7:12.7] [keggf:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG3906	2834632_fl_1	5684	19787	1548	516	YIR004W	375	6.0(10)-86	Saccharomyces cerevisiae	[ui:yir004w] [pn:similarity to caj1p, ydj1p and to dnaj1-like proteins:hypothetical 48.6 kd protein in bet1-pan1 intergenic region] [gn:yib4w] [gtcf:10.5:10.7:12.7] [keggf:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4172	9788936_c3_4	5685	19788	1461	487	YJL111W	1803	5.2(10)-186	Saccharomyces cerevisiae	[ui:yjl111w] [pn:component of chaperonin-containing t-complex:t-complex protein 1, eta subunit:tcp-1-eta:cct-eta] [gn:cct7:j0804] [gtcf:10.5:10.7:12.7] [keggf:14.2] [sgdfc:6.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5775	23829512_c2_26	5686	19789	2079	693	YJL034W	2374	1.6(10)-246	Saccharomyces cerevisiae	[ui:yjl034w] [pn:nuclear fusion protein:78 kd glucose regulated protein homolog precursor:grp78:immunoglobulin heavy chain binding protein homolog:bip] [gn:kar2:ssd1:grp78:j1248] [gtcf:10.5:10.7:11.1:12.16:12.7:12.8] [keggf:14.2] [
CONTIG5204	21522577_c2_4	5687	19790	1590	530	YJL014W	2030	4.5(10)-210	Saccharomyces cerevisiae	[ui:yjl014w] [pn:chaperonin of the tcp1 ring complex, cytosolic:t-complex protein 1, gamma subunit:tcp-1- gamma:cct-gamma] [gn:cct3:tcp3:bin2:j1336] [gtcf:10.5:10.7:12.7] [keggf:14.2] [sgdfc:6.1.0:9.2.0] [db:gtc-saccharomyces cerevi

CONTIG2981	24024074_c1_6	5688	19791	1473	491	YJL008C	1546	8.9(10)-159	Saccharomyces cerevisiae	[ui:yj1008c] [pn:component of chaperonin-containing t-complex-t-complex protein 1, theta subunit:tcp-1-theta:cct- theta] [gn:cct8:j1374] [gtcf:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5230	22672051_c1_13	5689	19792	1701	567	YJR064W	2039	5.0(10)-211	Saccharomyces cerevisiae	[ui:yjr064w] [pn:t-complex protein 1, epsilon subunit:tcp-1- epsilon:cct5:j1752] [gtcf:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5289	267012_f1_2	5690	19793	477	159	YJR097W	264	6.2(10)-23	Saccharomyces cerevisiae	[ui:yjr097w] [pn:weak similarity to caj1p:hypothetical 20.0 kd protein in acr1-yuh1 intergenic region] [gn:j1931] [gtcf:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4803	10171900_c1_8	5691	19794	2055	685	YKL073W	692	2.7(10)-68	Saccharomyces cerevisiae	[ui:ykl073w] [pn:chaperone of the er lumen:heat shock protein 70 homolog hsl precursor] [gn:hsl:ykl355] [gtcf:12.7:12.16:11.1] [keggfc:14.2] [sgdfc:6.1.0:6.2.0:9.4.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3857	4103453_f1_1	5692	19795	1107	369	YLR449W	476	8.0(10)-62	Saccharomyces cerevisiae	[ui:yrlr449w] [pn:strong similarity to peptidylprolyl isomerase fpr3p] [gtcf:10.5:10.7:12.7] [keggfc:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG862	20431663_13_2	5693	19796	564	188	YLR449W	95	0.023	Saccharomyces cerevisiae	[ui:ylr449w] [pn:strong similarity to peptidylprolyl isomerase fpr3p] [gtcf:10.5:10.7:12.7] [keggf:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3583	30660886_13_3	5694	19797	288	96	YMR161W	251	1.5(10)-21	Saccharomyces cerevisiae	[ui:ymr161w] [pn:similarity to dnaj proteins:hij1 protein] [gn:hij1:ym8520] [gtcf:10.5:10.7:12.7] [keggf:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4414	24390652_11_1	5695	19798	357	119	YNL227C	280	8.0(10)-24	Saccharomyces cerevisiae	[ui:ynl227c] [pn:weak similarity to dnaj-like proteins:hypothetical 68.8 kd protein in ure2-ssu72 intergenic region] [gn:n1254] [gtcf:10.5:10.7:12.7] [keggf:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4414	23923442_12_3	5696	19799	1299	433	YNL227C	247	1.5(10)-41	Saccharomyces cerevisiae	[ui:ynl227c] [pn:weak similarity to dnaj-like proteins:hypothetical 68.8 kd protein in ure2-ssu72 intergenic region] [gn:n1254] [gtcf:10.5:10.7:12.7] [keggf:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1898	15022061_12_2	5697	19800	918	306	YOR288C	452	7.5(10)-43	Saccharomyces cerevisiae	[ui:yor288c] [pn:disulfide isomerase related protein] [gn:mpd1] [gtcf:10.11:2.7] [keggf:14.2] [sgdfc:6.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5499	12_c3_13	5698	19801	1992	664	YDR341C	1345	2.8(10)-209	Saccharomyces cerevisiae	[ui:ydr341c] [pn:strong similarity to arginine-tRNA ligase] [gtcf:10.6] [keggf:14.2] [sgdfc:5.4.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5735	26798200_c1_13	5699	19802	642	214	YOL097C	690	4.5(10)-68	Saccharomyces cerevisiae	[ui:yol097c] [pn:tryptophan--trna ligase] [gn:wrs1] [gdcf:10.6] [keggf:14.2] [sgdcf:5.4.0.9.2.0] [db:gdc-saccharomyces cerevisiae]
CONTIG5735	26196061_c2_18	5700	19803	768	256	YOL097C	1010	5.5(10)-102	Saccharomyces cerevisiae	[ui:yol097c] [pn:tryptophan--trna ligase] [gn:wrs1] [gdcf:10.6] [keggf:14.2] [sgdcf:5.4.0.9.2.0] [db:gdc-saccharomyces cerevisiae]
CONTIG2571	24501442_f2_2	5701	19804	1308	436	YHR006W	393	1.3(10)-36	Saccharomyces cerevisiae	[ui:yhr006w] [pn:involved in pre-trna splicing:putative 60.8 kd zinc finger protein in gpal-erg1 intergenic region] [gn:stp2] [gdcf:10.6] [keggf:14.2] [sgdcf:4.5.0] [db:gdc-saccharomyces cerevisiae]
CONTIG5303	9957192_c1_10	5702	19805	1329	443	YHR006W	354	3.2(10)-32	Saccharomyces cerevisiae	[ui:yhr006w] [pn:involved in pre-trna splicing:putative 60.8 kd zinc finger protein in gpal-erg1 intergenic region] [gn:stp2] [gdcf:10.6] [keggf:14.2] [sgdcf:4.5.0] [db:gdc-saccharomyces cerevisiae]
CONTIG5764	4895137_c3_31	5703	19806	1182	394	YHR006W	119	0.00023	Saccharomyces cerevisiae	[ui:yhr006w] [pn:involved in pre-trna splicing:putative 60.8 kd zinc finger protein in gpal-erg1 intergenic region] [gn:stp2] [gdcf:10.6] [keggf:14.2] [sgdcf:4.5.0] [db:gdc-saccharomyces cerevisiae]
CONTIG4159	79186_f1_1	5704	19807	774	258	YHR163W	497	1.3(10)-47	Saccharomyces cerevisiae	[ui:yhr163w] [pn:weak multicopy suppressor of los1-1:protein] [gn:sol3] [gdcf:10.6] [keggf:14.2] [sgdcf:4.5.0] [db:gdc-saccharomyces cerevisiae]

CONTIG5654	4735640_c3_17	5705	19808	1371	457	YLR375W	249	1.5(10)-20	Saccharomyces cerevisiae	[ui:ylr375w] [pn:involved in pre-tRNA splicing and in uptake of branched-chain amino acids] [gn:stp3] [gtcf:10.6:12.1] [keggf:14.2] [sgdf:1.1.3.4.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4402	24489005_c1_4	5706	19809	1104	368	YNR034W	894	6.9(10)-100	Saccharomyces cerevisiae	[ui:ynr034w] [pn:multicopy suppressor of los1-1:sol1 protein] [gn:sol1:n3291] [gtcf:10.6] [keggf:14.2] [sgdf:4.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5140	4688933_c3_12	5707	19810	744	248	YOL102C	371	2.8(10)-34	Saccharomyces cerevisiae	[ui:yol102c] [pn:tma 2"-phosphotransferase] [gn:tpt1] [gtcf:10.6] [keggf:14.2] [sgdf:4.5.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5385	4492160_c2_12	5708	19811	1260	420	YFR010W	663	3.2(10)-65	Saccharomyces cerevisiae	[ui:yfr010w] [pn:similarity to c.elegans trna-guanine transglycosylase:putative ubiquitin carboxyl-terminal hydrolase yfr010w:ubiquitin thiolesterase:ubiquitin-specific processing protease:deubiquitinating enzyme] [gtcf:10.6:10.11] [
CONTIG2795	36110408_c3_7	5709	19812	648	216	YGL105W	542	2.2(10)-52	Saccharomyces cerevisiae	[ui:ygl105w] [pn:protein with specific affinity for g4 quadruplex nucleic acids:gu4 nucleic-binding protein 1:p42:arc1 protein] [gn:g4pl:arc1:g3085] [gtcf:10.6] [keggf:14.2] [sgdf:4.6.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5624	26360285_f2_4	5710	19813	525	175	YGL105W	266	3.8(10)-23	Saccharomyces cerevisiae	[ui:yg105w] [pn:protein with specific affinity for g4 quadruplex nucleic acids:gu4 nucleic-binding protein 1:p42:arc1 protein] [gn:g4p1:arc1:g3085] [gtcf:10.6] [keggf:14.2] [sgdfc:4.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG990	4768913_f2_1	5711	19814	690	230	YGL105W	191	1.2(10)-14	Saccharomyces cerevisiae	[ui:yg105w] [pn:protein with specific affinity for g4 quadruplex nucleic acids:gu4 nucleic-binding protein 1:p42:arc1 protein] [gn:g4p1:arc1:g3085] [gtcf:10.6] [keggf:14.2] [sgdfc:4.6.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3516	23849143_c2_7	5712	19815	714	238	YAL003W	529	5.2(10)-51	Saccharomyces cerevisiae	[ui:yal003w] [pn:translation elongation factor eef1beta:elongation factor 1-beta:ef-1-beta] [gn:efb1:tef5] [gtcf:10.7] [keggf:14.2] [sgdfc:5.2.0-9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG292	14875252_f2_2	5713	19816	525	175	YBL091C	173	9.5(10)-13	Saccharomyces cerevisiae	[ui:ybl091c] [pn:methionine aminopeptidase, isoform 2:methionine aminopeptidase 2:metap 2:peptidase m 2] [gn:map2:ybl0701] [gtcf:10.7] [ec:3.4.11.18] [keggf:14.1] [sgdfc:5.2.0:6.3.0] [db:gtc-saccharomyces cerevisiae]

CONTIG4487	16828377_f3_1	5714	19817	1323	441	YBL091C	1062	1.7(10)-107	Saccharomyces cerevisiae	[ui:ybl091c] [pn:methionine aminopeptidase, isoform 2:methionine aminopeptidase 2:metap 2:peptidase m 2] [gn:map2:ybl0701] [gicfc:10.7] [ec:3.4.11.18] [keggfc:14.1] [sgdgc:5.2.0:6.3.0] [db:gtc-saccharomyces cerevisiae]
CONTIG3041	36362805_f1_2	5715	19818	615	205	YBR118W	923	9.3(10)-93	Saccharomyces cerevisiae	[ui:ybr118w] [pn:translation elongation factor eef1 alpha-a chain, cytosolic:elongation factor 1-alpha:ef-1-alpha] [gn:tef2:ybr0913:tefl:p9513] [gicfc:10.7] [keggfc:14.2] [sgdgc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5539	36362805_f1_2	5716	19819	1383	461	YBR118W	2083	1.1(10)-215	Saccharomyces cerevisiae	[ui:ybr118w] [pn:translation elongation factor eef1 alpha-a chain, cytosolic:elongation factor 1-alpha:ef-1-alpha] [gn:tef2:ybr0913:tefl:p9513] [gicfc:10.7] [keggfc:14.2] [sgdgc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5583	4964037_c2_16	5717	19820	1320	440	YBR143C	1766	4.2(10)-182	Saccharomyces cerevisiae	[ui:ybr143c] [pn:translational release factor:eukaryotic peptide chain release factor subunit 1:erf1:omnipotent suppressor protein 1] [gn:sup1:sup45:sal4:ybr1120] [gicfc:10.7] [keggfc:14.2] [sgdgc:5.2.0:9.2.0] [db:gtc-saccharomyces ce

CONTIG5804	21928252_c3_69	5718	19821	1086	362	YDL084W	1542	2.3(10)-158	Saccharomyces cerevisiae	[ui:ydl084w] [pn:strong similarity to nuclear rna helicase:dead family] [gtcf:10.7] [keggf:14.2] [sgdfc:5.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5804	5250252_c2_56	5719	19822	201	67	YDL084W	189	3.2(10)-14	Saccharomyces cerevisiae	[ui:ydl084w] [pn:strong similarity to nuclear rna helicase:dead family] [gtcf:10.7] [keggf:14.2] [sgdfc:5.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5421	26600300_c2_10	5720	19823	1206	402	YDR021W	1323	3.7(10)-135	Saccharomyces cerevisiae	[ui:ydr021w] [pn:strong similarity to human translation initiation factor eif4a homolog] [gtcf:10.7] [keggf:14.2] [sgdfc:5.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG228	7276031_f3_3	5721	19824	477	159	YDR172W	117	3.7(10)-6	Saccharomyces cerevisiae	[ui:ydr172w] [pn:eukaryotic peptide chain release factor gip-binding subunit:erf2:omnipotent suppressor protein 2:erf3:erf-3:g1 to s phase transition protein 1] [gn:sup2:sup35:suf12:gst1:sal3:pmn 2:yd9395] [gtcf:10.7:12.8] [keggf:14.
CONTIG2600	433217_f1_1	5722	19825	420	140	YDR172W	129	1.8(10)-7	Saccharomyces cerevisiae	[ui:ydr172w] [pn:eukaryotic peptide chain release factor gip-binding subunit:erf2:omnipotent suppressor protein 2:erf3:erf-3:g1 to s phase transition protein 1] [gn:sup2:sup35:suf12:gst1:sal3:pmn 2:yd9395] [gtcf:10.7:12.8] [keggf:14.

CONTIG2600	22290936_f2_3	5723	19826	534	178	YDR172W	386	3.6(10)-35	Saccharomyces cerevisiae	[ui:ydr172w] [pn:eukaryotic peptide chain release factor gtp-binding subunit:erf2:omnipotent suppressor protein 2:erf3:erf3:g1 to s phase transition protein 1] [gn:sup2:sup35:suf1 2:gst1:sal3:pnm 2:yd9395] [gtcf:10.7:12.8] [keggfc:14.
CONTIG2600	36032263_f3_5	5724	19827	192	64	YDR172W	300	8.0(10)-26	Saccharomyces cerevisiae	[ui:ydr172w] [pn:eukaryotic peptide chain release factor gtp-binding subunit:erf2:omnipotent suppressor protein 2:erf3:erf3:g1 to s phase transition protein 1] [gn:sup2:sup35:suf1 2:gst1:sal3:pnm 2:yd9395] [gtcf:10.7:12.8] [keggfc:14.
CONTIG2600	9970452_f3_6	5725	19828	831	277	YDR172W	1032	2.6(10)-104	Saccharomyces cerevisiae	[ui:ydr172w] [pn:eukaryotic peptide chain release factor gtp-binding subunit:erf2:omnipotent suppressor protein 2:erf3:erf3:g1 to s phase transition protein 1] [gn:sup2:sup35:suf1 2:gst1:sal3:pnm 2:yd9395] [gtcf:10.7:12.8] [keggfc:14.
CONTIG5345	14711558_c3_21	5726	19829	2163	721	YDR211W	1422	1.2(10)-145	Saccharomyces cerevisiae	[ui:ydr211w] [pn:translation initiation factor eif2b epsilon, 81 kda subunit:translation initiation factor eif-2b- epsilon subunit:eif-2b gdp-gtp exchange factor:guanine nucleotide exchange factor subunit gcd6:gcd complex subunit gcd6]

CONTIG5306	10641063_c3_16	5727	19830	1458	486	YDR385W	2139	1.3(10)-221	Saccharomyces cerevisiae	[ui:ydr385w] [pn:translation elongation factor eef2:elongation factor 2:ef-2] [gn:eft2:eft1:o3317] [gtcf:10.7] [keggfc:14.2] [sgdfe:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5306	5100713_c3_15	5728	19831	714	238	YDR385W	1011	4.4(10)-102	Saccharomyces cerevisiae	[ui:ydr385w] [pn:translation elongation factor eef2:elongation factor 2:ef-2] [gn:eft2:eft1:o3317] [gtcf:10.7] [keggfc:14.2] [sgdfe:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5306	6672140_c2_12	5729	19832	426	142	YDR385W	620	1.2(10)-60	Saccharomyces cerevisiae	[ui:ydr385w] [pn:translation elongation factor eef2:elongation factor 2:ef-2] [gn:eft2:eft1:o3317] [gtcf:10.7] [keggfc:14.2] [sgdfe:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4326	25391536_f1_2	5730	19833	462	154	YEL034W	674	2.2(10)-66	Saccharomyces cerevisiae	[ui:yel034w] [pn:translation initiation factor eif5a.1:initiation factor 5a-2:eif-5a:eif-4d:hypusine containing protein hp2] [gn:hyp2:tif51a:sygp-ort21] [gtcf:10.7] [keggfc:14.2] [sgdfe:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG5665	20400292_f2_4	5731	19834	1596	532	YER025W	2098	2.7(10)-217	Saccharomyces cerevisiae	[ui:yer025w] [pn:translation initiation factor eif2 gamma chain:translational initiation factor 2 gamma subunit:eif-2- gamma] [gn:ged11] [gtcf:10.7] [keggfc:14.2] [sgdfe:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5017	24414661_c3_7	5732	19835	1200	400	YGL169W	850	1.1(10)-103	Saccharomyces cerevisiae	[ui:ygl169w] [pn:translation initiation protein: sua5 protein] [gn: sua5:g1660] [gtcf:10.7] [keggf:14.2] [sgdfc:5.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2627	26367752_f2_1	5733	19836	645	215	YGL094C	501	6.2(10)-47	Saccharomyces cerevisiae	[ui:ygl094c] [pn:component of pab1p-stimulated poly:a-ribonuclease:pab-dependent poly:a-specific ribonuclease subunit:pab1p-dependent poly:a-nuclease] [gn:pan2] [gtcf:10.7:10.9] [ec:3.1.13.4] [keggf:14.1] [sgdfc:4.10.0:5.2.0] [db:gt
CONTIG3648	210892_c3_6	5734	19837	945	315	YGL094C	171	2.1(10)-15	Saccharomyces cerevisiae	[ui:ygl094c] [pn:component of pab1p-stimulated poly:a-ribonuclease:pab-dependent poly:a-specific ribonuclease subunit:pab1p-dependent poly:a-nuclease] [gn:pan2] [gtcf:10.7:10.9] [ec:3.1.13.4] [keggf:14.1] [sgdfc:4.10.0:5.2.0] [db:gt
CONTIG3648	21492182_c3_5	5735	19838	804	268	YGL094C	311	1.3(10)-26	Saccharomyces cerevisiae	[ui:ygl094c] [pn:component of pab1p-stimulated poly:a-ribonuclease:pab-dependent poly:a-specific ribonuclease subunit:pab1p-dependent poly:a-nuclease] [gn:pan2] [gtcf:10.7:10.9] [ec:3.1.13.4] [keggf:14.1] [sgdfc:4.10.0:5.2.0] [db:gt

CONTIG2402	16519663_f2_1	5736	19839	1809	603	YGL049C	627	2.8(10)-73	Saccharomyces cerevisiae	[ui:ygl049c] [pn:mrna cap-binding protein:eif4f, 130k subunit:eukaryotic initiation factor 4f subunit p130:eif-4f:mrna cap-binding protein complex subunit p130] [gn:tif4632] [gtcf:10.7] [keggf:14.2] [sgdfc:5.2.0.9.2.0] [db:gtc-sacch]
CONTIG5035	5937562_c1_11	5737	19840	1563	521	YGR083C	567	3.0(10)-60	Saccharomyces cerevisiae	[ui:ygr083c] [pn:translation initiation factor eif2b, 71 kda:delta subunit:translation initiation factor eif-2b delta subunit:eif-2b gdp-gtp exchange factor:guanine nucleotide exchange factor subunit gcd2:gcd complex subunit gcd2] [gn:
CONTIG5278	23470005_f1_1	5738	19841	1221	407	YJL138C	1491	6.0(10)-153	Saccharomyces cerevisiae	[ui:yjl138c] [pn:translation initiation factor eif4a:translation initiation factor 4a:eukaryotic initiation factor 4a:eif-4a:stimulator factor i 37 kd component:p37] [gn:tifl:tif2:j0660] [gtcf:10.7] [keggf:14.2] [sgdfc:5.2.0.9.2.0]
CONTIG4464	24641888_c2_7	5739	19842	531	177	YJR007W	462	6.5(10)-44	Saccharomyces cerevisiae	[ui:yjr007w] [pn:translation initiation factor eif2, alpha chain:translational initiation factor 2 alpha subunit:eif- 2-alpha] [gn:sui2:j1429] [gtcf:10.7:1.1] [keggf:14.2] [sgdfc:5.2.0.9.1.0] [db:gtc-saccharomyces cerevisiae]

CONTIG5702	13947217_c1_20	5740	19843	357	119	YJR007W	437	2.8(10)-41	Saccharomyces cerevisiae	[ui:yjr007w] [pn:translation initiation factor eif2, alpha chain:translational initiation factor 2 alpha subunit:eif- 2-alpha] [gn:sui2:j1429] [gtcf:10.7:1.1] [keggc:14.2] [sgdfc:5.2.0:9.1.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2481	4785900_fl_1	5741	19844	615	205	YKL173W	413	1.3(10)-37	Saccharomyces cerevisiae	[ui:ykl173w] [pn:similarity to elongation factor 2 efl1:gin10 protein] [gn:gin10:ykl637] [gtcf:10.7] [keggc:14.2] [sgdfc:5.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG2814	26610288_f2_2	5742	19845	1557	519	YKL173W	433	6.9(10)-57	Saccharomyces cerevisiae	[ui:ykl173w] [pn:similarity to elongation factor 2 efl1:gin10 protein] [gn:gin10:ykl637] [gtcf:10.7] [keggc:14.2] [sgdfc:5.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG4289	33593750_fl_2	5743	19846	690	230	YKL081W	283	6.0(10)-25	Saccharomyces cerevisiae	[ui:ykl081w] [pn:translation elongation factor eef1, gamma chain:elongation factor 1-gamma 2:ef-1-gamma 2] [gn:tef4:efc1] [gtcf:10.7] [keggc:14.2] [sgdfc:5.2.0:9.2.0] [db:gtc-saccharomyces cerevisiae]
CONTIG1883	23882758_c2_5	5744	19847	276	92	YKR026C	235	7.5(10)-20	Saccharomyces cerevisiae	[ui:ykr026c] [pn:translation initiation factor eif2b, 34 kd, alpha subunit:translation initiation factor eif-2b alpha subunit:eif-2b gdp-gtp exchange factor:guanine nucleotide complex subunit gcn3:gcd complex subunit gcn3:trans